

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2004, 17:36:30 ; Search time 6138 Seconds
(without alignments)
11651.991 Million cell updates/sec

Title: US-10-036-150-44
Perfect score: 2395
Sequence: 1 cctggagcggagcgccgc.....gcaataattgagaaaaaaa 2395

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

EST :

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_est3.*

12: gb_est4.*

13: gb_est5.*

14: gb_est6.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_man.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_pmg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	710.8	29.7	1201	13	BX377108
C 2	706.4	29.5	723	14	CA308767
C 3	704.6	29.4	731	13	BU622377
4	698.6	29.2	935	12	BI771815

5	682.6	28.5	825	14	CF594116
6	662.2	27.6	809	12	BG171457
7	655.6	27.4	905	13	BU191836
8	646.4	27.0	971	14	CF593551
C 9	557.2	23.3	585	12	BQ001548
10	554.2	23.1	615	9	AL703949
11	519.2	21.7	801	12	BG742889
12	513.8	21.5	1089	12	BM920390
13	458.4	19.1	909	14	CD517899
14	439.8	18.4	546	9	AL698226
C 15	434.6	18.1	441	9	AI521101
C 16	405	16.9	418	28	AQ673215
C 17	395.2	16.5	434	10	BE549374
C 18	388.8	16.2	1201	13	BX377107
C 19	371.8	15.5	390	13	BX097186
20	370.8	15.5	640	13	BU425116
21	355.2	14.8	920	12	BG336024
22	355.2	14.8	970	12	BG336399
23	335	14.0	557	10	BE757899
C 24	312.2	13.0	368	10	AW265224
C 25	309.2	12.9	332	12	BM844459
26	308.4	12.9	595	12	BG346870
27	304	12.7	570	10	BE669243
C 28	303.6	12.7	405	10	AW262485
29	300.8	12.6	739	14	CA377408
C 30	300.6	12.6	319	9	AA687924
31	291.6	12.2	412	12	BM107678
32	280.8	11.7	631	9	AL871903
33	276.8	11.6	753	12	BI913095
34	264.2	11.0	508	14	CB783017
35	263	11.0	674	12	BG927822
36	248.4	10.4	418	14	CB765650
37	239	10.0	510	14	CB548333
38	237.4	9.9	253	9	AA361388
39	216.4	9.0	253	14	T32542
C 40	206.2	8.6	350	13	BQ293001
41	206	8.6	976	14	CD516167
42	205	8.6	1205	10	BF791461
43	204	8.5	318	14	Z44206
44	199	8.3	1099	12	BM455257
C 45	192.4	8.0	789	12	BG389289
46	184	7.7	318	12	BI051441
47	177	7.4	806	12	BG923173
48	177	7.4	3150	11	BC051059
49	172.6	7.2	355	10	BF746141
C 50	165.2	6.9	264	12	BI026475
51	163.4	6.8	764	13	BX077539
52	162.4	6.8	501	29	CG592530
53	160.4	6.7	252	9	AA356939
54	152.8	6.4	739	13	BU130677
C 55	150.6	6.3	517	12	BI391754
56	135.2	5.6	744	13	BX077538
57	116.4	4.9	460	10	BF442617
58	112.6	4.7	510	9	AL913388
59	110.4	4.6	720	29	CE024824
60	107.4	4.5	122	13	BQ360060
61	107.4	4.5	934	12	BE897861
62	106.8	4.5	556	12	BM523673
63	106.8	4.5	651	13	BQ522572
64	102	4.3	466	28	BZ270849
65	101.8	4.3	990	12	BM468049
66	101.8	4.3	2495	11	BC036916
67	101.8	4.3	3270	29	AY408630
68	101.2	4.2	758	12	BI080925
C 69	99.4	4.2	560	12	BI434815
70	96.6	4.0	880	14	CD387014
71	96.2	4.0	3270	29	AY408631
72	93.8	3.9	545	10	AW862654
73	90.6	3.8	3282	29	AY408632
74	89	3.7	124	10	BE685541
75	87.8	3.7	929	14	CD733602
76	87.4	3.6	929	13	BU151896
C 77	86.8	3.6	608	28	BZ296288

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BM920390 AGENCOURT
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BQ360060 MR3-HN016
BE897861 601440532
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BQ522572 NISC-nl17
BZ270849 CH230-509
BM468049 AGENCOURT
BC036916 Homo sapi
AY408630 Homo sapi
BI080925 602878836
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CD387014 AGENCOURT
AY408631 Pan trogl
AM862654 RLF09 Rat
AY408632 Mus muscu
BE685541 187887 MA
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BU151896 AGENCOURT
BZ296288 CGI966.r1

us-10-036-150-44.rst

Fri Aug 6 10:49:40 2004

78	85	927	13	BUL07863	BUL07863	602954132	151	42.4	1.8	677	10	B9654609
79	83.6	3.5	12	BJ002551	BJ002551	BJ002551	152	42.2	1.8	1201	13	BX396032
80	83.4	3.5	12	BJ102458	BJ102458	60288812	153	42	1.8	645	29	CNS01213
81	83.2	3.5	12	BU237135	BU237135	603410865	154	42	1.8	925	29	CNS0091P
82	82	3.4	798	BU237135	BU237135	603410865	155	41.6	1.7	401	28	AQ845931
83	82	3.4	837	BU237135	BU237135	603410865	156	41.6	1.7	515	13	BX424977
84	82	3.4	842	BU237135	BU237135	603410865	157	41.4	1.7	1201	9	AL531027
85	80.4	3.4	914	BU237135	BU237135	603410865	158	41.4	1.7	1201	13	BX381961
86	80.2	3.3	891	BU237135	BU237135	603410865	159	41.2	1.7	473	28	AZ050509
87	78.2	3.3	773	BU237135	BU237135	603410865	160	41.2	1.7	554	28	BH197929
88	77.2	3.2	807	BU237135	BU237135	603410865	161	41.2	1.7	565	28	BH195242
89	77	3.2	652	BU237135	BU237135	603410865	162	41.2	1.7	603	12	B1631378
90	76.6	3.2	922	BU237135	BU237135	603410865	163	41.2	1.7	644	9	AL107888
91	74.2	3.1	3578	BU237135	BU237135	603410865	164	41.2	1.7	671	12	B1605387
92	74.2	3.1	689	BU237135	BU237135	603410865	165	41	1.7	951	9	AL555760
93	74.2	3.1	981	BU237135	BU237135	603410865	166	40.8	1.7	962	13	BX415131
94	73.8	3.1	765	BU237135	BU237135	603410865	167	40.2	1.7	762	14	CB738088
95	72.2	3.0	789	BU237135	BU237135	603410865	168	40.2	1.7	505	13	BU664768
96	71.6	3.0	490	BU237135	BU237135	603410865	169	40.2	1.7	696	13	BY733512
97	70.8	3.0	528	BU237135	BU237135	603410865	170	40.2	1.7	723	28	AQ362027
98	69.8	2.9	585	BU237135	BU237135	603410865	171	40.2	1.7	785	28	AQ344174
99	67.4	2.8	625	BU237135	BU237135	603410865	172	40.2	1.7	994	13	BX414650
100	67.4	2.8	905	BU237135	BU237135	603410865	173	40.2	1.7	1026	28	BZ569417
101	66.8	2.8	959	BU237135	BU237135	603410865	174	40.2	1.7	1171	13	BX342087
102	66.6	2.8	606	BU237135	BU237135	603410865	175	40.2	1.7	1201	13	BX360624
103	66.6	2.8	941	BU237135	BU237135	603410865	176	40	1.7	884	13	BQ947303
104	64.8	2.7	378	BU237135	BU237135	603410865	177	40	1.7	887	9	AL524426
105	64.4	2.7	817	BU237135	BU237135	603410865	178	40	1.7	966	28	AZ675567
106	63.6	2.7	830	BU237135	BU237135	603410865	179	40	1.7	1200	13	BX415896
107	63.2	2.6	998	BU237135	BU237135	603410865	180	40	1.7	1201	13	BX381961
108	62.8	2.6	771	BU237135	BU237135	603410865	181	40	1.7	1201	13	BG759656
109	60.2	2.5	714	BU237135	BU237135	603410865	182	39.8	1.7	1000	13	BX407619
110	59.6	2.5	875	BU237135	BU237135	603410865	183	39.8	1.7	1093	13	BQ396664
111	59.2	2.5	884	BU237135	BU237135	603410865	184	39.8	1.7	1201	13	BX406090
112	59.2	2.5	684	BU237135	BU237135	603410865	185	39.6	1.7	665	12	B1625905
113	58.6	2.4	435	BU237135	BU237135	603410865	186	39.6	1.7	754	13	BUI05063
114	58.6	2.4	576	BU237135	BU237135	603410865	187	39.6	1.7	844	29	CNS0052P
115	58.6	2.4	636	BU237135	BU237135	603410865	188	39.6	1.7	898	13	BX390870
116	58.6	2.4	724	BU237135	BU237135	603410865	189	39.6	1.7	904	29	CNS0662Y
117	57.2	2.4	285	BU237135	BU237135	603410865	190	39.4	1.6	507	28	AQ682429
118	55.4	2.3	216	BU237135	BU237135	603410865	191	39.4	1.6	599	12	BM566094
119	54.8	2.3	911	BU237135	BU237135	603410865	192	39.4	1.6	831	12	B1755336
120	53.8	2.2	400	BU237135	BU237135	603410865	193	39.4	1.6	1126	13	BX446391
121	52.8	2.2	1019	BU237135	BU237135	603410865	194	39.2	1.6	652	14	CA297260
122	52.2	2.2	572	BU237135	BU237135	603410865	195	39.2	1.6	661	14	CA285706
123	52.2	2.2	666	BU237135	BU237135	603410865	196	39.2	1.6	699	14	CA285594
124	51	2.1	413	BU237135	BU237135	603410865	197	39.2	1.6	768	14	CA272154
125	50.8	2.1	681	BU237135	BU237135	603410865	198	39.2	1.6	928	10	BF206830
126	50.6	2.1	510	BU237135	BU237135	603410865	199	38.8	1.6	559	13	BX384405
127	50.2	2.1	651	BU237135	BU237135	603410865	200	38.8	1.6	474	28	BZ949684
128	49.6	2.0	776	BU237135	BU237135	603410865	201	38.8	1.6	552	13	BU497908
129	46.8	2.0	655	BU237135	BU237135	603410865	202	38.8	1.6	712	13	BX416727
130	46.8	2.0	961	BU237135	BU237135	603410865	203	38.8	1.6	1090	12	B1556767
131	46	1.9	807	BU237135	BU237135	603410865	204	38.8	1.6	1106	29	AG163789
132	45.6	1.9	993	BU237135	BU237135	603410865	205	38.8	1.6	1201	13	BX356664
133	45.2	1.9	542	BU237135	BU237135	603410865	206	38.6	1.6	325	29	CE817664
134	45.2	1.9	772	BU237135	BU237135	603410865	207	38.6	1.6	385	10	AM354542
135	44.4	1.9	383	BU237135	BU237135	603410865	208	38.6	1.6	706	29	CE696456
136	44.4	1.9	426	BU237135	BU237135	603410865	209	38.6	1.6	733	28	BZ092510
137	44.4	1.9	689	BU237135	BU237135	603410865	210	38.6	1.6	846	28	BZ092510
138	44.2	1.8	620	BU237135	BU237135	603410865	211	38.6	1.6	866	29	CNS010R
139	44.2	1.8	779	BU237135	BU237135	603410865	212	38.6	1.6	1077	29	CNS06996
140	44.2	1.8	1201	BU237135	BU237135	603410865	213	38.6	1.6	1155	13	BX444199
141	43.8	1.8	616	BU237135	BU237135	603410865	214	38.6	1.6	1159	29	CNS015XR
142	43.6	1.8	360	BU237135	BU237135	603410865	215	38.4	1.6	468	29	CE527691
143	43	1.8	651	BU237135	BU237135	603410865	216	38.4	1.6	672	28	BH88571
144	43	1.8	748	BU237135	BU237135	603410865	217	38.4	1.6	720	29	CE228270
145	43	1.8	779	BU237135	BU237135	603410865	218	38.4	1.6	765	28	B21303
146	43	1.8	781	BU237135	BU237135	603410865	219	38.4	1.6	894	28	AZ543408
147	43	1.8	839	BU237135	BU237135	603410865	220	38.4	1.6	902	29	CNS006QP
148	43	1.8	930	BU237135	BU237135	603410865	221	38.4	1.6	1201	29	CNS016BR
149	43	1.8	852	BU237135	BU237135	603410865	222	38.4	1.6	1451	10	BF688440
150	42.6	1.8	852	BU237135	BU237135	603410865	223	38.2	1.6	484	28	BZ906389

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AL053013 Drosophil
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BX424977 BX424977
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AZ050509 GSSTC1135
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CA285594 SCVPLB208
CA272154 SCVPLB208
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C 224	38.2	643	28	AZ312003	1.6	297	37.4	1.6	1425	11	BC018607	BC018607 Homo sapi
C 225	38.2	673	10	BE260998	1.6	298	37.4	1.6	2072	29	AV411198	AV411198 Homo sapi
C 226	38.2	736	28	BE2020145	1.6	299	37.2	1.6	431	13	BQ809016	BQ809016 1030008E1
C 227	38.2	744	14	CF869175	1.6	300	37.2	1.6	435	29	CE266826	CE266826 tigr-gss-
C 228	38.2	824	14	CF869301	1.6	301	37.2	1.6	454	10	BE761471	BE761471 894099D08
C 229	38.2	839	29	CNS004NB	1.6	302	37.2	1.6	456	9	AA962623	AA962623 om82D05.s
C 230	38.2	910	29	CNS006ON	1.6	303	37.2	1.6	541	14	CA200155	CA200155 SCRFL102
C 231	38.2	1201	29	CNS0141B	1.6	304	37.2	1.6	568	29	CE193316	CE193316 tigr-gss-
C 232	38	251	13	BF874248	1.6	305	37.2	1.6	629	12	BF873549	BF873549 963109F05
C 233	38	317	13	BE21843	1.6	306	37.2	1.6	642	29	CE647396	CE647396 tigr-gss-
C 234	38	538	29	CE409983	1.6	307	37.2	1.6	672	10	AW950474	AW950474 EST362544
C 235	38	1201	9	AL564081	1.6	308	37.2	1.6	672	13	BQ651153	BQ651153 1112091F0
C 236	38	1273	12	BQ256643	1.6	309	37.2	1.6	672	13	BQ815678	BQ815678 1030052B0
C 237	37.8	584	12	BM320685	1.6	310	37.2	1.6	721	12	BG860698	BG860698 1024072C1
C 238	37.8	879	12	BQ621829	1.6	311	37.2	1.6	746	12	BG845290	BG845290 1024009F0
C 239	37.8	922	13	BK462312	1.6	312	37.2	1.6	1201	9	AL524337	AL524337 AL524337
C 240	37.8	996	9	AL546967	1.6	313	37.2	1.6	1201	9	AL524338	AL524338 AL524338
C 241	37.8	1024	12	BG388919	1.6	314	37.2	1.6	1201	9	AL563716	AL563716 AL563716
C 242	37.8	1201	9	AL553735	1.6	315	37.2	1.6	1201	13	BX387714	BX387714 BX387714
C 243	37.6	508	12	B1531929	1.6	316	37	1.5	278	9	AL372209	AL372209 MCB487D01
C 244	37.6	646	28	A2636767	1.6	317	37	1.5	412	13	BY285359	BY285359 BY285359
C 245	37.6	692	12	BF136028	1.6	318	37	1.5	422	12	EM753262	EM753262 K-EST0030
C 246	37.6	840	28	BF136028	1.6	319	37	1.5	457	14	CF947432	CF947432 UI-D-GC1-
C 247	37.6	902	29	CNS00CVM	1.6	320	37	1.5	507	14	CD739626	CD739626 4028268 1
C 248	37.6	1028	13	BX376226	1.6	321	37	1.5	593	10	BE444849	BE444849 WHB1129 B
C 249	37.6	1101	29	CNS0039G	1.6	322	37	1.5	726	13	BX306217	BX306217 BX306217
C 250	37.6	1131	9	AL517123	1.6	323	37	1.5	761	13	BU271162	BU271162 603814887
C 251	37.6	1638	10	BF137817	1.6	324	37	1.5	859	12	CG240021	CG240021 OXGDL66TV
C 252	37.4	239	10	BF874262	1.6	325	37	1.5	859	12	B1857846	B1857846 603388406
C 253	37.4	247	28	BZ851677	1.6	326	37	1.5	874	12	BG755301	BG755301 602714044
C 254	37.4	294	13	BQ836079	1.6	327	37	1.5	884	13	BQ214135	BQ214135 AGENCOURT
C 255	37.4	322	10	AW114856	1.6	328	37	1.5	1004	29	CNS032TV	AL268060 Tetraodon
C 256	37.4	380	9	AT273765	1.6	329	37	1.5	1061	13	BX391246	BX391246 602257382
C 257	37.4	409	10	BF968022	1.6	330	37	1.5	1067	10	BF797585	BF797585 60391246
C 258	37.4	410	14	W12162	1.6	331	37	1.5	1109	29	AG129047	AG129047 Pan trogl
C 259	37.4	419	9	AL367917	1.6	332	37	1.5	1201	9	AL565971	AL565971 AL565971
C 260	37.4	421	9	AL273323	1.6	333	37	1.5	1201	13	BX360604	BX360604 BX360604
C 261	37.4	441	9	AA488481	1.6	334	37	1.5	1201	13	BX442961	BX442961 BX442961
C 262	37.4	446	9	AL304808	1.6	335	37	1.5	1201	13	BX444892	BX444892 BX444892
C 263	37.4	469	9	AL346735	1.6	336	36.8	1.5	455	14	CB741917	CB741917 AMGNNUC:M
C 264	37.4	528	14	CB123677	1.6	337	36.8	1.5	530	29	CE794563	CE794563 tigr-gss-
C 265	37.4	535	12	BM846845	1.6	338	36.8	1.5	575	29	DR26M24T	DR26M24T Danio rer
C 266	37.4	549	12	BM839796	1.6	339	36.8	1.5	625	29	BX189757	BX189757 Danio rer
C 267	37.4	575	10	BE257300	1.6	340	36.8	1.5	632	28	AZ640745	AZ640745 IM0502K23
C 268	37.4	580	28	BF715317	1.6	341	36.8	1.5	657	10	BB446136	BB446136 BB446136
C 269	37.4	616	10	BE252555	1.6	342	36.8	1.5	673	12	BQ058651	BQ058651 BQ058651
C 270	37.4	645	28	BM575576	1.6	343	36.8	1.5	861	12	BM416448	BM416448 OP21542 M
C 271	37.4	648	13	EX119057	1.6	344	36.8	1.5	912	12	B1103816	B1103816 602885678
C 272	37.4	680	12	BG491601	1.6	345	36.8	1.5	2486	11	AK051015	AK051015 Mus muscu
C 273	37.4	692	29	CNS007WH	1.6	346	36.6	1.5	394	29	CE213512	CE213512 tigr-gss-
C 274	37.4	702	10	BE253792	1.6	347	36.6	1.5	465	14	CD848707	CD848707 DH0AC0102
C 275	37.4	711	13	BX734048	1.6	348	36.6	1.5	529	13	BQ353960	BQ353960 PM0-HT091
C 276	37.4	715	14	CD348996	1.6	349	36.6	1.5	644	13	BQ813716	BQ813716 N014C03 P
C 277	37.4	841	12	B1087131	1.6	350	36.6	1.5	674	13	CA135098	CA135098 SCJLRT101
C 278	37.4	876	13	BQ644304	1.6	351	36.6	1.5	697	29	CE186464	CE186464 tigr-gss-
C 279	37.4	896	13	BU931047	1.6	352	36.6	1.5	706	28	AQ448154	AQ448154 mgx00017K
C 280	37.4	917	13	BQ889933	1.6	353	36.6	1.5	736	13	BU130913	BU130913 603117145
C 281	37.4	926	13	BQ500695	1.6	354	36.6	1.5	762	13	CA088556	CA088556 SCRFAM212
C 282	37.4	926	13	BQ52379	1.6	355	36.6	1.5	838	14	CF289958	CF289958 AGENCOURT
C 283	37.4	929	13	BQ53104	1.6	356	36.6	1.5	884	10	BF569519	BF569519 602186015
C 284	37.4	937	13	BQ650376	1.6	357	36.6	1.5	948	28	CC368521	CC368521 602186015
C 285	37.4	939	13	BQ877227	1.6	358	36.6	1.5	997	29	CNS005TE	AL060767 Drosophila
C 286	37.4	956	13	BQ651346	1.6	359	36.6	1.5	1026	13	BX354717	BX354717 BX354717
C 287	37.4	962	13	BX383763	1.6	360	36.6	1.5	1068	9	AL527496	AL527496 AL527496
C 288	37.4	1007	13	BQ056184	1.6	361	36.6	1.5	1163	9	AL577643	AL577643 AL577643
C 289	37.4	1021	12	BQ052974	1.6	362	36.6	1.5	1201	9	AL513905	AL513905 AL513905
C 290	37.4	1037	12	BM927940	1.6	363	36.6	1.5	499	12	BM694274	BM694274 UI-B-C11-
C 291	37.4	1045	12	BQ051836	1.6	364	36.4	1.5	606	13	BU327441	BU327441 603495111
C 292	37.4	1050	12	BM562665	1.6	365	36.4	1.5	647	12	B1392755	B1392755 pgin.pk0
C 293	37.4	1088	12	BM928461	1.6	366	36.4	1.5	693	12	BH012641	BH012641 TDGAM05TH
C 294	37.4	1098	13	BQ876947	1.6	367	36.4	1.5	727	28	CC587503	CC587503 CH240_385
C 295	37.4	1217	12	BM906870	1.6	368	36.4	1.5	729	29		
C 296	37.4	1227	12	BM913126	1.6	369	36.4	1.5				

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Fri Aug 6 10:49:40 2004

C 370	36.4	794	12	BG471870	BG471870 602513345	C 443	35.8	1.5	706	28	BZ805325	BZ805325 PUF6V61FD
C 371	36.4	816	28	BH552486	BH552486 BOGK72TF	444	35.8	1.5	707	11	AX110674	AX110674 Zea mays
C 372	36.4	833	28	BH440313	BH440313 BOGXE35TR	445	35.8	1.5	725	12	BG280612	BG280612 602780593
C 373	36.4	848	9	AL528948	AL528948 AL528948	446	35.8	1.5	833	28	CC415585	CC415585 PUEK841TD
C 374	36.4	1040	13	BX375588	BX375588 BX375588	447	35.8	1.5	870	13	BU305820	BU305820 603611480
C 375	36.4	1179	13	BX403696	BX403696 BX403696	448	35.8	1.5	877	14	CD328705	CD328705 AGENCOURT
C 376	36.4	1203	29	CNS015Y4	AL106084 DROBOPHIL	449	35.8	1.5	902	12	BM459710	BM459710 AGENCOURT
C 377	36.2	331	14	CF182006	CF182006 IOSD2F I	450	35.8	1.5	912	29	CG278321	CG278321 CG2AB85TV
C 378	36.2	552	28	AZ085485	AZ085485 RPCI-23-4	451	35.8	1.5	946	29	CG094044	CG094044 PUI1025TB
C 379	36.2	662	10	BE570838	BE570838 601329345	452	35.8	1.5	984	13	BX369944	BX369944 BX369944
C 380	36.2	796	13	BZ971078	BZ971078 PUGF088TB	453	35.8	1.5	990	29	AG041486	AG041486 Pan trogl
C 381	36.2	828	13	BU263851	BU263851 603815664	454	35.8	1.5	1041	29	AG042970	AG042970 Pan trogl
C 382	36.2	904	29	CNS00F2V	BZ970690 UT-M-FRO-	455	35.8	1.5	1068	9	AL549536	AL549536 AL549536
C 383	36.2	946	13	BX431296	AL070107 DROBOPHIL	456	35.8	1.5	1101	29	CNS016R4	AL144924 Anopheles
C 384	36.2	977	29	CNS00JX7	AL076850 DROBOPHIL	457	35.8	1.5	1108	29	CNS016R4	AL107098 Drosophil
C 385	36.2	1009	29	CNS010EW	AL098882 DROBOPHIL	458	35.8	1.5	1103	13	BX403654	AX403654 BX403654
C 386	36.2	1073	13	BQ073722	BQ073722 AGENCOURT	459	35.8	1.5	1200	13	BX339396	BX339396 BX339396
C 387	36.2	1201	9	AL538546	AL538546 AL538546	460	35.8	1.5	1391	11	AF318370	AF318370 Homo sapi
C 388	36.2	1201	13	BX394133	BX394133 BX394133	461	35.6	1.5	367	12	BG273600	BG273600 OV2 27 F1
C 389	36.2	1201	13	BX462261	BX462261 BX462261	462	35.6	1.5	456	9	AL450697	AL450697 AL450697
C 390	36.2	1201	13	BX462261	AL058374 RPCI-11-4	463	35.6	1.5	505	14	CD859582	CD859582 G15_001L1
C 391	36	279	28	AQ583874	AQ583874 RPCI-11-4	464	35.6	1.5	528	28	AQ412180	AQ412180 RPCI-11-1
C 392	36	379	10	BE293358	BE293358 601143788	465	35.6	1.5	551	10	BE808235	BE808235 213389 MA
C 393	36	401	28	AQ456822	AQ456822 HS 5153 A	466	35.6	1.5	554	12	BG649430	BG649430 EM1_79 CI
C 394	36	422	28	AZ830739	AZ830739 2M0110H11	467	35.6	1.5	578	12	BG733185	BG733185 346924 MA
C 395	36	435	10	BB821911	BB821911 BB821911	468	35.6	1.5	616	14	CD207639	CD207639 HS1_33 EO
C 396	36	503	28	BZ940143	BZ940143 CH240_107	469	35.6	1.5	640	14	CF489420	CF489420 POL1_57 B
C 397	36	512	13	BQ552616	BQ552616 H4017A05-	470	35.6	1.5	654	14	CD463636	CD463636 ETH1_45 E
C 398	36	541	14	CD694912	CD694912 EST11435	471	35.6	1.5	670	9	BQ989862	BQ989862 OGG20L17
C 399	36	566	12	BH788848	BH788848 fzm021f0	472	35.6	1.5	678	9	AL855511	AL855511 AL855511
C 400	36	586	13	CB8262	CB8262 C88262 Mous	473	35.6	1.5	699	29	CG954192	CG954192 MBEIX80TF
C 401	36	624	12	BM379926	BM379926 MEST54-B0	474	35.6	1.5	701	13	BQ535399	BQ535399 602563060
C 402	36	635	14	CB380742	CB380742 3529_1_24	475	35.6	1.5	710	13	BQ750606	BQ750606 EST633342
C 403	36	653	29	CS591764	CS591764 CH240_392	476	35.6	1.5	710	14	CF480132	CF480132 POL1_63 H
C 404	36	666	13	AW267379	AW267379 829001F08	477	35.6	1.5	841	29	CG293401	CG293401 OGWNF35TH
C 405	36	669	13	BH380717	BH380717 603860438	478	35.6	1.5	881	28	BH133926	BH133926 ENTNC94TF
C 406	36	753	28	BH662058	BH662058 BOMMU12TF	479	35.6	1.5	885	13	BX425603	BX425603 BX425603
C 407	36	773	12	BI765770	BI765770 603046528	480	35.6	1.5	894	29	CNS01591	AL105168 Drosophil
C 408	36	775	13	BU129977	BU129977 603118120	481	35.6	1.5	925	23	CNS0091P	AL053013 Drosophil
C 409	36	792	29	CG360302	CG360302 OGWJQ01TV	482	35.6	1.5	936	13	BU123103	BU123103 603148360
C 410	36	804	28	BH180602	BH180602 017_1_21-	483	35.6	1.5	953	13	BX383396	BX383396 AGENCOURT
C 411	36	805	28	BZ278574	BZ278574 CH230-308	484	35.6	1.5	956	13	BQ889234	BQ889234 AGENCOURT
C 412	36	837	12	BG754193	BG754193 OGUHL30TV	485	35.6	1.5	1080	29	AG146549	AG146549 Pan trogl
C 413	36	840	29	CG655714	CG655714 OGUHL30TV	486	35.6	1.5	1101	29	CNS000C9	AG146549 Pan trogl
C 414	36	867	29	CG047358	CG047358 PUFUS09TD	487	35.6	1.5	1101	29	CNS000BMG	AL065386 Drosophil
C 415	36	902	28	BZ579707	BZ579707 mah2_733-	488	35.6	1.5	1147	28	CC289353	CC289353 CH261-185
C 416	36	909	29	CNS02POE	AL208247 tetradon	489	35.6	1.5	1201	13	BX443397	BX443397 BX443397
C 417	36	927	12	BI906112	BI906112 603062512	490	35.6	1.5	1201	13	BX443397	AL057362 Drosophil
C 418	36	960	13	BX415111	BX415111 BX415111	491	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 419	36	1000	13	BX407619	BX407619 BX407619	492	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
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C 421	36	1181	9	BF206810	BF206810 601870206	494	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 422	36	1201	9	AL530352	AL530352 AL530352	495	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 423	36	1351	13	BQ955445	BQ955445 AGENCOURT	496	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 424	36	1351	13	BQ955445	BQ955445 AGENCOURT	497	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 425	36	1351	13	BQ955445	BQ955445 AGENCOURT	498	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 426	36	1351	13	BQ955445	BQ955445 AGENCOURT	499	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 427	36	1351	13	BQ955445	BQ955445 AGENCOURT	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
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C 429	36	1351	13	BQ955445	BQ955445 AGENCOURT	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 430	36	1351	13	BQ955445	BQ955445 AGENCOURT	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 431	35.8	325	12	BM019568	BM019568 603647788	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 432	35.8	339	29	CG772228	CG772228 CH240_801	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 433	35.8	370	9	AA865012	AA865012 cd93b11.s	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 434	35.8	370	9	AA865012	AA865012 cd93b11.s	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 435	35.8	403	9	AA190879	AA190879 zphsc05.s	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 436	35.8	448	10	CA871882	CA871882 TA04_1090	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 437	35.8	448	10	CA871882	CA871882 TA04_1090	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 438	35.8	473	13	BQ904708	BQ904708 Ta04_1090	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 439	35.8	554	29	CNS0421D	AL271534 Tetradon	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 440	35.8	573	12	BW743673	BW743673 K-BST0016	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 441	35.8	658	12	BW743673	BW743673 K-BST0016	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185
C 442	35.8	678	29	BX129833	BX129833 Danio rer	500	35.6	1.5	1201	13	BX443397	CC289353 CH261-185

ALIGNMENTS

RESULT 1	BX377108	BX377108 Homo sapiens	1201 bp	linear	EST 08-MAY-2003
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DEFINITION	BX377108	BX377108 Homo sapiens	1201 bp	linear	EST 08-MAY-2003
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VERSION	BX377108	BX377108 Homo sapiens	1201 bp	linear	EST 08-MAY-2003
KEYWORDS	BX377108	BX377108 Homo sapiens	1201 bp	linear	EST 08-MAY-2003
SOURCE	BX377108	BX377108 Homo sapiens	1201 bp	linear	EST 08-MAY-2003
ORGANISM	BX377108	BX377108 Homo sapiens	1201 bp	linear	EST 08-MAY-2003

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2614.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI002BC12QPL&cluster=2614.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI002BC12QPL.

FEATURES

Location/Qualifiers
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 29.7%; Score 710.8; DB 13; Length 1201;
Best Local Similarity 95.1%; Pred. No. 4.4e-190;
Matches 750; Conservative 4; Mismatches 33; Indels 3; Gaps 2;
QY 1599 GTGCAAGTGTGGCAGTGCCTCGACAGAGGGGCTCAGGAAGACGCTGAGCAGCCTT 1658
DB 48 GTCCGGAAATCCCGGATGCCCTGACAGAGGGGCTCAGGAAGACGCTGAGCAGCCTT 107
QY 1659 ATCCAGGCTCTGGGTGTCGACACAGGTGTTACATCTGTGCTGTCAGGTGAGTGC 1718
DB 108 ATCCAGGCTCTGGGTGTCGACACAGGTGTTACATCTGTGCTGTCAGGTGAGTGC 167
QY 1719 CTGAGTTCTTGGAAAGTAGTCTTCTCGACTGTTACCAAGTCAATGTAAGAGTGGC 1778
DB 168 CTCAGTTCTTGGAAAGTAGTCTTCTCGACTGTTACCAAGTCAATGTAAGAGTGGC 227
QY 1779 GGTCACAGAGAACAGCCCTCCAGCTGAGGGGTGTGTAAT--CGACAGCCTCCAG 1836
DB 228 GGTCACAGAGAACAGCCCTCCAGCTGAGGGGTGTGTAATTCGACAGGCTCCAG 287
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DB 348 GTCAAGAGAGACTTGGTGCCACTCATCTCTGCCACCCCAAGATGCATCTGCTCA 407
QY 1957 TCAGGTCCAGATTTCTTCCAGGCGGAGTTCCTGTGTTGGAATCTTAGTCTTGGCT 2016
DB 408 TCAGGTCCAGATTTCTTCCAGGCGGAGTTCCTGTGTTGGAATCTTAGTCTTGGCT 467
QY 2017 CGGACACTTCTATTCTTACGTGGGAGTGGTGGAGCAGTGAAGAGAGCGGATGG 2076
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QY 2137 TGGGCCCCCACCACCTGACAGCCCTCATCCCTCTTGGCTTGAGCCCTCAGAGGC 2196

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QY 2317 TCTGCTATTGAATTAGTACTAGCTGCACACAGTATGTTTACCAAGAAATAACCG 2376
Db 767 GYCTGCGATTGAATTAGTACTAGCTGCACACAGTATGTTTACCAAGAAATAACCG 826
QY 2377 CAATAATTG 2385
Db 827 CATATTG 835

RESULT 2

CA308767/c
LOCUS
DEFINITION
UI-H-Ftl-bhy-b-03-0-UI-s1 NCI CGAP Ftl Homo sapiens cDNA clone
723 bp mRNA linear EST 01-NOV-2002
ACCESSION
CA308767
VERSION
CA308767.1 GI:24471821
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 723)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers
1..723
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-Ftl-bhy-b-03-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ftl"
/note="Organ: Lung; Vector: p7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Ftl is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
p7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCATGCGG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.


```

Db      371  TTAGCTGGGAGTGTTGGTGAAGCAGTGAAGAAAGGCGGATGGTCAACCTCAGATCCAC 312
QY      2093  AGAGCCAGGATCAAGGAGCCCACTGAGTGGGAGGAGGAGTGTGGGCCCCCACCACCA 2152
Db      311  AGAGCCAGGATCAAGGAGCCCACTGAGTGGGAGGAGGAGTGTGGGCCCCCACCACCA 252
QY      2153  CCTGACAGCCCTCATCCCTCTTGGCTTGAAGCCCTGAGAGCCCTGTGCTGAGTGTCT 2212
Db      251  CCTGAGCAGCCCTCATCCCTCTTGGCTTGAAGCCCTGAGAGCCCTGTGCTGAGTGTCT 192
QY      2213  GACCGAGACACTCAGAGCTTTGTATCAGGAGCAGGCTTCTCGAGCAGGATGATCT 2272
Db      191  GACCGAGACACTCAGAGCTTTGTATCAGGAGCAGGCTTCTCGAGCAGGATGATCT 132
QY      2273  GTGCAACGCTTGCACTCGGGCCCATCTGGGCTCATGCTCTCTCTCTCTCTCTCTCTCT 2332
Db      131  GTGCAACGCTTGCACTCGGGCCCATCTGGGCTCATGCTCTCTCTCTCTCTCTCTCTCT 132
QY      2333  GTACTAGCTGACACAGTATGTATCTACCAAGAAATAAAGCGCAATAATTGAAATA 2392
Db      71  GTACTAGCTGACACAGTATGTATCTACCAAGAAATAAAGCGCAATAATTGAAATA 72
QY      2393  AAA 2395
Db      11  AAA 9

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RESULT 4
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LOCUS
DEFINITION
60305859F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5208023 5',
mRNA sequence.
BI771815
VERSION
BI771815.1 GI:15763393
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 935)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11521 row: n column: 24
High quality sequence stop: 780.

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FEATURES

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Location/Qualifiers
1..935
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5208023"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

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ORIGIN

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Query Match      29.2%; Score 698.6; DB 12; Length 935;
Best Local Similarity 97.9%; Pred. No. 1.2e-186;
Matches 761; Conservative 0; Mismatches 9; Indels 7; Gaps 5;

QY      15  CGCGGCTGCAGCAGGCGGAGGCTCCAGGTGGGCTGGTCCGCATCCAGCTAGCGTGC 74
Db      1  CGCGGCTGCAGCAGGCGGAGGCTCCAGGTGGGCTGGTCCGCATCCAGCTAGCGTGC 60
QY      75  CACGATCGGCTGGGCTCCGGACTTTTCGCTACCTGTTGCTAGCGATCAGGTGCTAG 134
Db      61  CACGATCGGCTGGGCTCCGGACTTTTCGCTACCTGTTGCTAGCGATCAGGTGCTAG 120
QY      135  GATCGCGGTCTTCCTTCGGGGATTCTCCGGCTCCGTTCTCTCTGCGCAGCGGA 194
Db      121  GATCGCGGTCTTCCTTCGGGGATTCTCCGGCTCCGTTCTCTCTGCGCAGCGGA 180
QY      195  ACAGGAGCGGAGCCCGCCAGCCGAACTTCGCTGGCTGGAGCCAGTTCTTAATCGAC 254
Db      181  ACAGGAGCGGAGCCCGCCAGCCGAACTTCGCTGGCTGGAGCCAGTTCTTAATCGAC 240
QY      255  GCTGCCACCACTCTCTTCAGTAAAGTTGTTTCTGATAGATGCTTGAGAGATGA 314
Db      241  GCTGCCACCACTCTCTTCAGTAAAGTTGTTTCTGATAGATGCTTGAGAGATGA 300
QY      315  TTTTGTGTTTGGGTCAAAGGTTGAAATTTATGCCCTACACAACTTACCTTTGGA 374
Db      301  TTTTGTGTTTGGGTCAAAGGTTGAAATTTATGCCCTACACAACTTACCTTTGGA 360
QY      375  AGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCACCTACAGTTACTATGCT 434
Db      361  AGGAGCATCTCACAGTTTGTGGCTGAAGCAAAAGCCACCTACAGTTACTATGCT 420
QY      435  CAAGGCATTGATGACGGGAGCCTTCTGGCTTTGTGAGCTCATCAGGACCTCAATTC 494
Db      421  CAAGGCATTGATGACGGGAGCCTTCTGGCTTTGTGAGCTCATCAGGACCTCAATTC 480
QY      495  TCCTGCACCTCTGGAAGACAGTGTGATAGCAAGCAAGAGAGCTGGAAGAAAGAT 554
Db      481  TCCTGCACCTCTGGAAGACAGTGTGATAGCAAGCAAGAGAGCTGGAAGAAAGAT 540
QY      555  CTTTATGAGAGATGAAACCTGGGTTAAATTTATCCCAAGCAATTTGTGGAATAT 614
Db      541  CTTTATGAGAGATGAAACCTGGGTTAAATTTATCCCAAGCAATTTGTGGAATAT 599
QY      615  AACACCTCATTTTTCGTGTAGATACAGAGGTGGATATAATAATGTACAGAGGCA 674
Db      600  AACACCTCATTTTTCGTGTAGATACAGAGGTGGATATAATAATGTACAGAGGCA 659
QY      675  GGATAAAA--GTATTAAAGAGGAGATTGGGACATATT--AATCCTCCTACCTGGG 731
Db      660  GGATAAAAGTATTAAACAGAGAGATTGGGACATATTAAATCCTCCTACCTGGG 719
QY      732  GGACCAACA--TTGGCCACATTTTCAGGCGCCCAACA--GCCCTGATTGGCAGAG 785
Db      720  GGACCAACAATTGGCCACATTTTCAGGCGCCCAACAAGCCCTCGATTGGGCAAG 776

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RESULT 5

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CF594116
LOCUS
DEFINITION
AGENCOURT 15622192 NIH_MGC_147 Homo sapiens cDNA clone
IMAGE:30528044 5', mRNA sequence.
CF594116
ACCESSION
CF594116.1 GI:36348285
VERSION
CF594116.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 825)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

```

Fri Aug 6 10:49:40 2004

JOURNAL
COMMENT

Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue procurement: Dr. Stefan Hansson
cDNA library preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: NDAM613 row: f column: 21
High quality sequence stop: 628.
Location/Qualifiers

FEATURES
source

1. .825
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30528044"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
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5'-TTTTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

ORIGIN

Query Match 28.5%; Score 682.6; DB 14; Length 825;
Best Local Similarity 95.9%; Pred. No. 3.9e-182;
Matches 722; Conservative 0; Mismatches 29; Indels 2; Gaps 2;

QY 1 CTGTGAGCGGAGCGCGCTGCAGAGCGGCGGCTCCAGGTGGGGTGGTTCGGCATC 60
DB 66 CTGTGAGCGGAGCGCGCTGCAGAGCGGCGGCTCCAGGTGGGGTGGTTCGGCATC 125
QY 61 CAGCCTAGCGTGCACAGATGCGGCTGGGCTCCGGGACTTTCCTACCTGTTCCGTAGCG 120
DB 126 CAGCCTAGCGTGCACAGATGCGGCTGGGCTCCGGGACTTTCCTACCTGTTCCGTAGCG 185
QY 121 ATCGAGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCCTCCGGGCTCCGTTCCGTTCC 180
DB 186 ATCGAGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCCTCCGGGCTCCGTTCCGTTCC 245
QY 181 TCTGCCAGAGCGGAACACGAGCGGAGCCCGCCAGCCCGCAACCCCTCGGCTGGAGCCAGT 240
DB 246 TCTGCCAGAGCGGAACACGAGCGGAGCCCGCCAGCCCGCAACCCCTCGGCTGGAGCCAGT 305
QY 241 TCTAACCTGGACACCGCTGCCACCACTCTCTTCAGTAAAGTTGTTATGTTCTCATAGAT 300
DB 306 TCTAACCTGGACACCGCTGCCACCACTCTCTTCAGTAAAGTTGTTATGTTCTCATAGAT 365
QY 301 GCCTTGAGAGATGATTTTGTGTTGGTCAAGGGTGTGAATTTATGCCCTACACAACT 360
DB 366 GCCTTGAGAGATGATTTTGTGTTGGTCAAGGGTGTGAATTTATGCCCTACACAACT 425
QY 361 TACCTTGTGAAAAGGAGCATCTCACAGTTTGTGGCTGAGCAAGCAACCCCTACAGTT 420
DB 426 TACCTTGTGAAAAGGAGCATCTCACAGTTTGTGGCTGAGCAAGCAACCCCTACAGTT 485
QY 421 ACTATGCTCGAATCAAGGCAATGATGACGCGGAGCCTTCTCGCTTGTGCAAGCTCATC 480
DB 486 ACTATGCTCGAATCAAGGCAATGATGACGCGGAGCCTTCTCGCTTGTGCAAGCTCATC 545
QY 481 AGGAACCTCAATTCCTCTCTGCTGGAAGACAGTGTGATGAACAGCAAGCAAGCAGCT 540

DB 546 AGGAACCTCAATTCCTCTGCACTGCTGGAAGACAGCTGTGATAAGACAAGCAAGCAGCT 605
QY 541 GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGTTAAATTTATCCAAAGCATTTT 600
DB 606 GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGTTAAATTTATCCAAAGCATTTT 665
QY 601 GTGGAATATGATGGAAACACCTCATTTTCGTGTCAGATTACACAGAGTGGATATAAT 660
DB 666 GTGGAATATGATGGAAACACCTCATTTTCGTGTCAGATTACACAGAGTGGATATAAT 725
QY 661 GTCAAG-AGGCAATTTGGATAAAGTATT-AAAAAGAGGAGATTGGGACATATTAACTCTCC 718
DB 726 GTCAAGAGGCAATTTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAACTCTCC 785
QY 719 ACTACCTGGGGCTGGACCAATTTGGCCATTT 751
DB 786 TTCACCTACCTGGGGCTGGACCAATTT 818

RESULT 6

BGI71457 809 bp mRNA linear EST 06-FEB-2001
LOCUS 602321972F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4425448 5',
DEFINITION mRNA sequence.

ACCESSION BGI71457
VERSION BGI71457.1 GI:12678160
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 809)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM10170 row: o column: 17
High quality sequence stop: 653.

FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4425448"
/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_89"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dt primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 27.6%; Score 662.2; DB 12; Length 809;
Best Local Similarity 95.7%; Pred. No. 2.4e-176;
Matches 734; Conservative 0; Mismatches 28; Indels 5; Gaps 5;
QY 173 TTGCTTCTCTGCCAGAGCGGAACACGGA-GGGAGGCCCGCCAGCCGACCTCG-GC 230
DB 1 TTGCTTCTCTGCCAGAGCGGAACACGGAACCGGACCGGAGCCCGCCAGCCGACCTCGTC 60
QY 231 TGGAGCCAGTTCTAATCTGACCACTGCGCACCTCTCTTTCAGTAAAGTTGTTATGTT 290

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Db      61  TGGAGCCAGTTCTAACTGGACCAGCTGGCCACCACCTCTCTTCAGTAAAGTTCTATTGT 120
QY      291  TCTGATPAGATGCTTCTGAGAGATGATTTGTTGTTGGTCAAGAGGTTGTAATTTATGCC 350
Db      121  TCTGATPAGATGCTTCTGAGAGATGATTTGTTGTTGGTCAAGAGGTTGTAATTTATGCC 180
QY      351  CTACACAACTTACCTTGTGGAAAAAGAGAGCATCTACAGTTTGTGGCTGAAGCAAGCC 410
Db      181  CTACACAACTTACCTTGTGGAAAAAGAGAGCATCTACAGTTTGTGGCTGAAGCAAGCC 240
QY      411  ACCTACAGTTACTATGCTTCTGATCAAGGATGTATGACGGGAGCCTTCTGGCTTTGT 470
Db      241  ACCTACAGTTACTATGCTTCTGATCAAGGATGTATGACGGGAGCCTTCTGGCTTTGT 300
QY      471  CGAGCTCATCAGAACTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 530
Db      301  CGAGCTCATCAGAACTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY      531  AAAAGCAGCTGAAAAAGAAATAGTCTTTTATGGAGATGAAACCTGCTGCTGCTGCTGCT 590
Db      361  AAAAGCAGCTGAAAAAGAAATAGTCTTTTATGGAGATGAAACCTGCTGCTGCTGCTGCT 420
QY      591  AAAGCATTTTGTGGAATATGATGGAACAACTCAATTTTGTGTCAGATTACACAGAGGT 650
Db      421  AAAGCATTTTGTGGAATATGATGGAACAACTCAATTTTGTGTCAGATTACACAGAGGT 480
QY      651  GGATAATAATGTACAGAGGCAATTTGGATAAAGTATTAAGAGAGAGATTGGGACATTT 710
Db      481  GGATAATAATGTACAGAGGCAATTTGGATAAAGTATTAAGAGAGAGATTGGGACATTT 540
QY      711  AATCCTCACTACCTGGGCTGGACCAATTTGGCCACATTTGAGGCGCCACAGCCCTCT 770
Db      541  AATCCTCACTACCTGGGCTGGACCAATTTGGCCACATTTGAGGCGCCACAGCCCTCT 600
QY      771  GATTGGCAGAGCTGAGCAGATGGACAGCTGCTGATGAAGATCCACACTCACTGCA 830
Db      601  GATTGGCAGAGCTGAGCAGATGGACAGCTGCTGATGAAGATCCACACTCACTGCA 659
QY      831  GTCGAAGGAG-AGAGAGACGCTTTTACCAATTTGCTGCTGCTGCTGCTGCTGCTGCT 888
Db      660  GTCGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
QY      889  ATGCTGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 935
Db      720  TTGTTGCAACGCGCTCCCGGCGCTCCTCAGCAAGAGAGAGAGAGAGAGAGAGAGAG 766

RESULT 7
LOCUS   BU191836
DEFINITION   AGENCOURT_7779796 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6019801
5', mRNA sequence.
ACCESSION   BU191836
VERSION     BU191836.1 GI:22705820
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLNL13222 row: o column: 02

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            /clone="IMAGE:6019801"
            /tissue_type="epithelioid carcinoma"
            /lab_host="PH10B (phage-resistant)"
            /clone_lib="NIH_MGC_70"
            /note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 1.1 kb. Library constructed by Life
            Technologies."

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ORIGIN
Query Match      27.4%; Score 655.6; DB 13; Length 905;
Best Local Similarity 96.3%; Pred. No. 1.9e-174;
Matches 704; Conservative 0; Mismatches 20; Indels 7; Gaps 3;

QY      640  TACACAGAGGTGGATAATAATGTCACGAGGCAATTTGGATAAAGTATTAAGAGAGAGAT 699
Db      1   TACACAGAGGTGGATAATAATGTCACGAGGCAATTTGGATAAAGTATTAAGAGAGAGAT 60
QY      700  TGGGACATATTAATCCTCCACTACTCTGGGCTGGACCAATTTGGCCACATTTGAGGGCCC 759
Db      61  TGGGACATATTAATCCTCCACTACTCTGGGCTGGACCAATTTGGCCACATTTGAGGGCCC 120
QY      760  AACAGCCCTCGATTGGGCGAAGCTGACGAGATGACAGCGTCTGATCAAGATCCAC 819
Db      121  AACAGCCCTCGATTGGGCGAAGCTGACGAGATGACAGCGTCTGATCAAGATCCAC 180
QY      820  ACCTCACTGAGTCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
Db      181  ACCTCACTGAGTCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY      880  GACCATGGCATGCTGAAAACAGGAAGTCACGGGCGCTCTCCACGAGGAGGTTGAATACA 939
Db      241  GACCATGGCATGCTGAAAACAGGAAGTCACGGGCGCTCTCCACGAGGAGGTTGAATACA 300
QY      940  CCTCTGATTTAATCAGTTCTGCTTTGAAAAGAAACCCGGTGATATCCGACATCCAAAG 999
Db      301  CCTCTGATTTAATCAGTTCTGCTTTGAAAAGAAACCCGGTGATATCCGACATCCAAAG 360
QY      1000  CACGTCCAATAGACGATGCTGCGACACTCGGACATCGGACATCGGCTTACCGATTCCA 1059
Db      361  CACGTCCAACAGACGATGCTGCGACACTCGGACATCGGCTTACCGATTCCA 420
QY      1060  AAAGCAGTGTAGGAGCCTCTCTATTTCCAGTTGTGGAAGAGAACCAATGAGAGAGCAG 1119
Db      421  AAAGCAGTGTAGGAGCCTCTCTATTTCCAGTTGTGGAAGAGAACCAATGAGAGAGCAG 480
QY      1120  TTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTGCAAGAGATGTGCGG 1179
Db      481  TTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTGCAAGAGATGTGCGG 540
QY      1180  TCATATGAAAAAGATCCTGGGTTTTCAGCAGTTTAAATGTTCAGAAAGATTGATGGAAAC 1239
Db      541  TCATATGAAAAAGATCCTGGGTTTTCAGCAGTTTAAATGTTCAGAAAGATTGATGGAAAC 600
QY      1240  TGGATCAGACTGTACTTGGAGGAAAGCATTCAGAAAGTCTTATTCACCTGGGCTCCAG 1299
Db      601  TGGATCAGACTGTACTTGGAGGAAAGCATTCAGAAAGTCTTATTCACCTGGGCTCCAA 660
QY      1300  GTTCTC---AGGAGTACCTGGATGCTCT---GAAGACGCTGAGCTT-GTCCCTGAGTGC 1352
Db      661  GGGTTCTCAGGCGAGTACCTGGGATGGCTCTGAGAAACGCTGAGCTTGGTCCCTGAGTGC 720
QY      1353  ACAAGTGGCCC 1363
Db      721  ACAAGTGGGCC 731

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Fri Aug 6 10:49:40 2004

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RESULT 8
CF593551
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM621 row: b column: 18
High quality sequence stop: 651.
Location/Qualifiers
1. 971
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30531017"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 147"
/note="Organ: Placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamHI; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTT-3', size-selected for average
insert size 2.3 kb and normalized to 10^5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."
ORIGIN
Query Match 27.0%; Score 646.4; DB 14; Length 971;
Best Local Similarity 99.8%; Pred. No. 8.3e-172;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCTGAGCCGGAAGCGGGTGCAGCGGCGAGGCTCCAGGTGGGTGGTCCGCATC 60
DB 44 CCTGAGCCGGAAGCGGGTGCAGCGGCGAGGCTCCAGGTGGGTGGTCCGCATC 103
QY 61 CAGCCTAGCGGTGCCAGATCGGCTGGGCTCCGGGACTTTTCGCTACTCTGTGCGTAGCG 120
DB 104 CAGCCTAGCGGTGCCAGATCGGCTGGGCTCCGGGACTTTTCGCTACTCTGTGCGTAGCG 163
QY 121 ATCCAGGTGCTAGGATCGCGGTCTTCTCTCGGGGATTCCTCCGGGCTCCGGTTCGTTCC 180
DB 164 ATCCAGGTGCTAGGATCGCGGTCTTCTCTCGGGGATTCCTCCGGGCTCCGGTTCGTTCC 223
QY 181 TCTGCCAGCGGGAACAGCGAGCGAGCCCGAGCCCGGACCTCCGCTGGAGCCAGT 240
DB 224 TCTGCCAGCGGGAACAGCGAGCGAGCCCGAGCCCGGACCTCCGCTGGAGCCAGT 283
QY 241 TCTAACTGGACACGCTGCCACCTCTCTTTCAGTAAAGTTGTTTGTCTGATAGAT 300

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DB 284 TCTAACTGGACACGCTGCCACCTCTCTTTCAGTAAAGTTGTTTGTCTGATAGAT 343
QY 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAAGGTGTGAATTTATGCTCCCTACCAACT 360
DB 344 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAAGGTGTGAATTTATGCTCCCTACCAACT 403
QY 361 TACCTTTGTGAAAAAGAGAGCATCTCACAGTTTTTGTGGCTGAAAGCAAGCCACTACAGTT 420
DB 404 TACCTTTGTGAAAAAGAGAGCATCTCACAGTTTTTGTGGCTGAAAGCAAGCCACTACAGTT 463
QY 421 ACTATGCTCGAATCAAGGCATTGATGAGGGGAGCCTTCTCGGCTTTGTGCGAGTCATC 480
DB 464 ACTATGCTCGAATCAAGGCATTGATGAGGGGAGCCTTCTCGGCTTTGTGCGAGTCATC 523
QY 481 AGGAACCTCAATTTCTCTGCACCTGCTGGAAGACAGTGTGATAAGACAAAGCAAGCAGCT 540
DB 524 AGGAACCTCAATTTCTCTGCACCTGCTGGAAGACAGTGTGATAAGACAAAGCAAGCAGCT 583
QY 541 GGAAGAAAGATAGTCTTTTATGAGATGAACCTGGGTTAAATTTATCCCAAGCAATTT 600
DB 584 GGAAGAAAGATAGTCTTTTATGAGATGAACCTGGGTTAAATTTATCCCAAGCAATTT 643
QY 601 GTGGAATATGATGGAACCAACCTCATTTTCTGTCAGATTACACAGAG 648
DB 644 GTGGAATATGATGGAACCAACCTCATTTTCTGTCAGATTACACAGAG 691

RESULT 9
BQ001548
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1. 585
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5893229"
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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP DH1"
/note="Organ: Lung; Vector: pVT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoRI; Site 2: Not I;
NCI CGAP DH1 is a normalized cDNA library containing the
following tissue(s): VS-8 Cell line from Metastatic
Chondrosarcoma in Lung. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoRI adaptor, digested

```

with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTCG.

TAG_ISSUE=lung
TAG_LIB=UI-H-DH1
TAG_SEQ=AGATCATTCG

ORIGIN

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Query Match      23.3%; Score 557.2; DB 12; Length 585;
Best Local Similarity 98.6%; Pred. No. 1.5e-146;
Matches 562; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1826 CAGCTCCAGCAGAGGTTGGAGCTGCAGCTGGGGAAGAGAGACATCGGCTGGA 1885
Db 585 CAGCTCCAGCAGAGGTTGGAGCTGCAGCTGGGGAAGAGAGACATCGGCTGGA 526
QY 1886 CACTCAGAGGGTCAAAAGGAGACTTGGTCGACCACTCATCTGCCACCCCCAGAAATGC 1945
Db 525 CACTCAGAGGGTCAAAAGGAGACTTGGTCGACCACTCATCTGCCACCCCCAGAAATGC 466
QY 1946 ATCTGCTCATCAGCTCCAGATTCTTTCCAGGCGGAGCTTTCTCTGTGGAATCTTA 2005
Db 465 ATCTGCTCATCAGCTCCAGATTCTTTCCAGGCGGAGCTTTCTCTGTGGAATCTTA 406
QY 2006 GTCTTGGCTTCGGACACTTCATTCTGTAGCTGGGAGTGGTGGAGGAGTGAAGAA 2065
Db 405 GTCTTGGCTTCGGACACTTCATTCTGTAGCTGGGAGTGGTGGAGGAGTGAAGAA 346
QY 2066 GAGCGGATGGTCACTCAGATCCAGAGCCAGGATCAAGGACCCACTCGAGTGGC 2125
Db 345 GAGCGGATGGTCACTCAGATCCAGAGCCAGGATCAAGGACCCACTCGAGTGGC 286
QY 2126 AGCAGGACTCTGTGGCCCCCACCACCCCTGACAGCCCTCATCCCTCTTGGCTTGA 2185
Db 285 AGCAGGACTCTGTGGCCCCCACCACCCCTGACAGCCCTCATCCCTCTTGGCTTGA 226
QY 2186 CCTCAGAGCCCTGTGCTGAGTGTCTGACCGAGACTCAGAGCTTGTGTCATCAGGCA 2245
Db 225 CCTCAGAGCCCTGTGCTGAGTGTCTGACCGAGACTCAGAGCTTGTGTCATCAGGCA 166
QY 2246 CAGGCTTCCTCGAGGAGGATGATCTGTCACCGCTTGACCTCGGCGCCATCTGGCT 2305
Db 165 CAGGCTTCCTCGAGGAGGATGATCTGTCACCGCTTGACCTCGGCGCCATCTGGCT 106
QY 2306 CATGCTCTCTCTCTCTCTTGAATAGTACCTAGCTGACAGATGATGATGATACAA 2365
Db 105 CATGCTCTCTCTCTCTCTTGAATAGTACCTAGCTGACAGATGATGATGATACAA 46
QY 2366 AGAATAACGGCAATAATTGAGAAAAAAA 2395
Db 45 AGAATAACGGCAATAATTGAGTCTCAAA 16
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RESULT 10

AL703949

LOCUS

DEFINITION

DKEZp686F1428 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone

AL703949

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Unpublished (2001)

COMMENT

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by MediGenomix (Martinsried/Germany) within the cDNA

sequencing consortium of the German Genome Project. No sl sequence

available.

This clone (DKEZp686F1428) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.

FEATURES

source

1. 615

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKEZp686F1428"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: hlcc3)"

/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;

cDNA-collection"

ORIGIN

Query Match

Best Local Similarity

Matches 556; Conservative

23.1%; Score 554.2; DB 9; Length 615;

99.5%; Pred. No. 1.1e-145;

Mismatches 3; Indels 0; Gaps 0;

QY 230 CTGAGGCGAGTTCTAACTGGACCACTGCGCCACCTCTCTTCAGTAAAGTCTTATTG 289

Db 57 CAGGAGCGAGTTCTAACTGGACCACTGCGCCACCTCTCTTCAGTAAAGTCTTATTG 116

QY 290 TTCTGATAGTGCCTTGAGAGATGATTTGTGTTGGTCAAAAGGTTGTAATTTATGC 349

Db 117 TTCTGATAGTGCCTTGAGAGATGATTTGTGTTGGTCAAAAGGTTGTAATTTATGC 176

QY 350 CCTACACAACTTACCTTGTGGAAGGAGCATCTCAGTTTGTGGCTGAAGCAAGC 409

Db 177 CCTACACAACTTACCTTGTGGAAGGAGCATCTCAGTTTGTGGCTGAAGCAAGC 236

QY 410 CACTACAGTTACTATGCTCGAATCAAGGCATTTGATGCGGGAGCCTTCCTGGCTTG 469

Db 237 CACTACAGTTACTATGCTCGAATCAAGGCATTTGATGCGGGAGCCTTCCTGGCTTG 296

QY 470 TCGACCTCATCAGGACCTCAATTCCTGCACTGCTGGAAGACAGTGTGTAAGACAAG 529

Db 297 TCGACCTCATCAGGACCTCAATTCCTGCACTGCTGGAAGACAGTGTGTAAGACAAG 356

QY 530 CAAAAGCAGCTGGAAAAAGATAGTCTTTTATGGAGTGAACCTCAATTTTCGTGTCAGATTACAGAGG 649

Db 357 CAAAAGCAGCTGGAAAAAGATAGTCTTTTATGGAGTGAACCTCAATTTTCGTGTCAGATTACAGAGG 416

QY 590 CAAAGCATTGTGGAATATGATGGAACAACCTCAATTTTCGTGTCAGATTACAGAGG 649

Db 417 CAAAGCATTGTGGAATATGATGGAACAACCTCAATTTTCGTGTCAGATTACAGAGG 476

QY 650 TGGATAAATCTCAGAGGCAATTTGGATAAGTATTAAAAAGAGAGATTTGGGACATAT 709

Db 477 TGGATAAATCTCAGAGGCAATTTGGATAAGTATTAAAAAGAGAGATTTGGGACATAT 536

QY 710 TAATCTCTCCACTACCTGGGCTGGACCAATTTGGCCATTTTCAGGGCCCAACGCCCCC 769

Db 537 TAATCTCTCCACTACCTGGGCTGGACCAATTTGGCCATTTTCAGGGCCCAACGCCCCC 596

QY 770 TGATTGGGAGAGCTGAG 788

Db 597 TGATTGGGAGAGCTGAG 615

RESULT 11

BG742889

LOCUS

BG742889

801 bp

mRNA

linear

EST 15-MAY-2001

us-10-036-150-44.rst

Fri Aug 6 10:49:40 2004

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mRNA sequence.
ACCESSION BG742889
VERSION BG742889.1 GI:14053542
KEYWORDS EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 801)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMi0632 row: k column: 17
High quality sequence stop: 798.
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

Query Match 21.7%; Score 519.2; DB 12; Length 801;
Best Local Similarity 85.1%; Pred. No. 1.1e-135;
Matches 667; Conservative 0; Mismatches 23; Indels 94; Gaps 4;

QY 1167 ACAGATGTCGCGTCATATGAAAGACCTCTGGTTTGGAGCTTTAAATGTCAGAAAG 1226
D 12 AGAGATGTCGCGTCATATGAAAGACCTCTGGTTTGGAGCTTTAAATGTCAGAAAG 71
QY 1227 ATTGCATGGGAATGGATCAGCTTACTTGGAGAAAGCACTTCAAGAGTCTCTATCAA 1286
D 72 ATTGCATGGGAATGGATCAGCTTACTTGGAGAAAGCACTTCAAGAGTCTCTATCAA 131
QY 1287 CTTGGGCTCCAGGTTCTCAGGAGTACCTGGATGCTCTGAAGACGCTGAGTTCCT 1346
D 132 CTTGGGCTCCAGGTTCTCAGGAGTACCTGGATGCTCTGAAGACGCTGAGTTCCT 191
QY 1347 GAGTGCACAAAGTGCCTCA-----GTTCTCACTCCCTGCTCTCTGCT 1384
D 192 GAGTGCACAAAGTGCCTCACTTATTCATGATGCTTCTCACTCCCTGCTCTGCT 251
QY 1385 CAGGCTCCACAGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACTGTCATCTCTGG 1444
D 252 CAGGCTCCACAGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACTGTCATCTCTGG 311
QY 1445 GTTTCTCTGCTCTTTATTTGGTGATCCTGGTTCTTTTGGCGGCTTCACTGATGCTG 1504
D 312 GTTTCTCTGCTCTTTATTTGGTGATCCTGGTTCTTTTGGCGGCTTCACTGATGCTG 371
QY 1505 CACCTCAGCTGAAAGTTCGTGCTTCTGTCCTCTGTCGCTGCGGCGGAGGCTGCT 1564
D 372 CACCTCAGCTGAAAGTTCGTGCTTCTGTCCTCTGTCGCTGCGGCGGAGGCTGCT 431
QY 1565 TTCGTT----- 1570
D 432 GATGCTGCTGGGCTCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 491

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1571 -----TACCAGACTCTGTTGAACACCTGTTGTGTGTCGCAAGTCTCTGGCA 1614
D 492 GGGTGGAAACACCCCAAGAGACTCTGTTGAACACCTGTTGTGTGTCGCAAGTCTCTGGCA 551
QY 1615 GTGCCCTGGACAGAGGGGCTCAGGGAAGCACTGAGCAGCCTTATCCAGGCCTCTGGG 1674
D 552 GTGCCCTGGACAGAGGGGCTCAGGGAAGCACTGAGCAGCCTTATCCAGGCCTCTGGG 611
QY 1675 TGTCCCGACACAGAGTGTTCACATCTGTGTGTGTCAGTGCAGTCCCTCAGTCTTGTGAAAG 1734
D 612 TGTCCCGACACAGAGTGTTCACATCTGTGTGTGTCAGTGCAGTCCCTCAGTCTTGTGAAAG 671
QY 1735 CTAGGTTCTCGGACTGTTACCAAGTGTATTAAGAGCTGGCGGTCA-CAGAGGAACA 1793
D 672 CTAGGTTCTCGGACTGTTACCAAGTGTATTAAGAGCTGGCGGTCA-CAGAGGAACA 731
QY 1794 AGCCCCCAGCTCA-GGGGTGTGTAATCGGACAGCCTCCAGCAGAGGTGTGGAGCT 1852
D 732 AGCCCCCAGCTCA-GGGGTGTGTAATCGGACAGCCTCCAGCAGAGGTGTGGAGCT 791
QY 1853 GCAG 1856
D 792 GCAG 795

RESULT 12
BM920390 1089 bp mRNA linear EST 12-MAR-2002
LOCUS AGENCOURT 6709592 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750347
DEFINITION 5', mRNA sequence.
ACCESSION BM920390
VERSION BM920390.1 GI:19370769
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1089)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12781 row: c column: 20
High quality sequence stop: 693.
Location/Qualifiers
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/mol_type="mRNA"
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/clone_lib="NIH_MGC_122"
/Note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

FEATURES
source

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ORIGIN

Query Match 21.5%; Score 513.8; DB 12; Length 1089;
Best Local Similarity 69.6%; Pred. No. 4.5e-134;
Matches 953; Conservative 0; Mismatches 14; Indels 402; Gaps 3;

QY 1 CCTGGAGCCGGAAGCGCGCTGACAGAGCGAGGCTCCAGGTGGGTCCGATC 60
DB 19 CCTGGAGCCGGAAGCGCGCTGACAGAGCGAGGCTCCAGGTGGGTCCGATC 78
QY 61 CAGCCTAGCGTGTCCACGATCGCGCTGGGCTCGGACCTTCCTACCTGTCGAGCG 120
DB 79 CAGCCTAGCGTGTCCACGATCGCGCTGGGCTCGGACCTTCCTACCTGTCGAGCG 138
QY 121 ATCAGGCTGCTAGGATCGCGTCTCTTCCTTCGGGGATCTTCCTCGGCTCCGCTTCCTCC 180
DB 139 ATCAGGCTGCTAGGATCGCGTCTCTTCCTTCGGGGATCTTCCTCGGCTCCGCTTCCTCC 198
QY 181 TCTGCCAGAGCGGAACACAGGAGCGGAGCCCGCAGCCCGGAGCCCTCGGCTGGAGCAGT 240
DB 199 TCTGCCAGAGCGGAACACAGGAGCGGAGCCCGCAGCCCGGAGCCCTCGGCTGGAGCAGT 258
QY 241 TCTAACTGGACACCGCTGCCACCTCTCTTCCTTCAGTAAAGTGTGTAATTTATGCCCTACCAACT 360
DB 259 TCTAACTGGACACCGCTGCCACCTCTCTTCCTTCAGTAAAGTGTGTAATTTATGCCCTACCAACT 378
QY 301 GCCTTGAGAGATGATTTGTGTTGGTCAAGGGGTGTGAATTTATGCCCTACCAACT 360
DB 319 GCCTTGAGAGATGATTTGTGTTGGTCAAGGGGTGTGAATTTATGCCCTACCAACT 378
QY 361 TACCTTGTGAAAAGGAGCAGTCTACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT 420
DB 379 TACCTTGTGAAAAGGAGCAGTCTACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT 438
QY 421 ACTATGCTCGAATCAAGGCAATGATGAGCGGGAGCCTTCCTGGCTTTGTGAGTCAATC 480
DB 439 ACTATGCTCGAATC----- 453
QY 481 AGGAACCTCAATTCCTCTGCACTGCTGGAAGACAGTGTGATGAACAGCAAGCAAGCAGCT 540
DB 454 ----- 453
QY 541 GGAAGAAAGATAGTCTTTTATGGAGATGAACCTGGGTAAATTAATTTCCCAAGCAATTT 600
DB 454 ----- 453
QY 601 GTGGAATATGATGAACCAACCTCATTTTTCGTGTGATGATGATGATGATGATGATGATGAT 660
DB 454 ----- 453
QY 661 GTCACAGGCAATTTGGATAAAGTATTAAGAGAGAGATGGGACATATTAATCCTCCAC 720
DB 454 ----- 453
QY 721 TACCTGGGCTGGACCAATTTGCCACATTTAGGGCCCAAGAGCCCTGATTTGGGAG 780
DB 454 ----- 453
QY 781 AAGCTGAGGAGATGAGACAGCGTGTGATGAATCCACCTCACTGAGTCGAGGAG 840
DB 454 -----AAGGAG 459
QY 841 AGAGAGCGCTTTTACCAATTTGCTGTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 900
DB 460 AGAGAGCGCTTTTACCAATTTGCTGTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 519
QY 901 GGAAGTCAAGGCGCTCTCTCCACGAGGAGTGAATACACCTCTGATTTAATCAGTTCT 960
DB 520 GGAAGTCAAGGCGCTCTCTCCACGAGGAGTGAATACACCTCTGATTTAATCAGTTCT 579
QY 961 GCGTTTGAAGAAACCGGTGATATCGACATCCAAAGCAGCTCCAAATAGACGAGTGTG 1020
DB 580 GCGTTTGAAGAAACCGGTGATATCGACATCCAAAGCAGCTCCAAATAGACGAGTGTG 639
QY 1021 GCTGCGACTGGCGATAGACATGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 1080

DB 640 GCTGCGACTGGCGATAGACATGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 699
QY 1081 CTATTTCCAGTTGTGAAGGAAGCAACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
DB 700 CTATTTCCAGTTGTGAAGGAAGCAACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 759
QY 1141 ACAGTGCAGCTTAGTAACTGTTGCAAGAGATGTGCCGTTCATATGAAAAGATCCTGGG 1200
DB 760 ACAGTGCAGCTTAGTAACTGTTGCAAGAGATGTGCCGTTCATATGAAAAGATCCTGGG 819
QY 1201 TTTGAGCAGTTTAAATGTCAAGAGATGTGCAAGAGATGTGCCGTTCATATGAAAAGATCCTGGG 1260
DB 820 TTTGAGCAGTTTAAATGTCAAGAGATGTGCAAGAGATGTGCCGTTCATATGAAAAGATCCTGGG 879
QY 1261 GAAAAGCATTCAAGAGTCTTATCAACCTCGGGCTCCAGGTTCTCAGGAGTACCTGG-A 1319
DB 880 GAAAAGCATTCAAGAGTCTTATCAACCTCGGGCTCCAGGTTCTCAGGAGTACCTGGNA 937
QY 1320 TGCTCTGAAGAGCGTGGCTTCTCCTGAGTGCACAGTGGCCAGTTTC 1368
DB 938 TGCTCTGAGAGCGTGGCTTCTCCTGAGTGCACAGTGGCCAGTTTC 986

RESULT 13
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LOCUS
DEFINITION
AGENCOURT 14364490 NIH MGC 181 Homo sapiens cDNA clone
IMAGE:30397358 5', mRNA sequence.
ACCESSION
CD517899
VERSION
CD517899.1 GI:31449617
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 909)
NIH-MGC <http://mgi.nci.nih.gov/>.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Contact: Daniela S. Gerhard, Ph.D.
COMMENT
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: ND4W480 row: 1 column: 15
High quality sequence stop: 688.

FEATURES
source

1..909
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30397358"
/tissue_type="White Matter"
/dev_stage="Unknown"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_181"
/note="Vector: pCMV-Sport6.1; Site 1: NotI; Site 2: EcoRV
(destroyed); Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.42 kb. Library was constructed by
(Invitrogen). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 19.1%; Score 458.4; DB 14; Length 909;
Best Local Similarity 82.0%; Pred. No. 2.3e-118;

Query Match	18.1%	Score 434.6	DB 9	Length 441	
Best Local Similarity	99.1%	Pred. No. 9.8e-112			
Matches 437	Conservative	0	Mismatches 4	Indels 0	Gaps 0
QY	1947	TCCTGGCTCATCAGGTCAGATTCTTTTCCAAAGCGGACGCTTTTCTGTGTGGAATTCCTTAG	2006		
Db	441	TCCTGGCTCATCAGGTCAGATTCTTTTCCAAAGCGGACGCTTTTCTGTGTGGAATTCCTTAG	382		
QY	2007	TCCTTGGCTTCGGACACCTTCATTTCGTTAGCTCGGGAGTCGTCGAGGAGTCAGTGAAG	2066		
Db	381	TCCTTGGCTTCGGACACCTTCATTTCGTTAGCTCGGGAGTCGTCGAGGAGTCAGTGAAG	322		
QY	2067	AGSCGGATGTCACACTCAGATCCACAGAGCCAGGATCAAGGAGCCCACTGCAGCTGGCA	2126		
Db	321	AGSCGGATGTCACACTCAGATCCACAGAGCCAGGATCAAGGAGCCCACTGCAGCTGGCA	262		
QY	2127	GCAGGACTGTGGGCCCCCAACCCCTGCACAGCCCTCATCCCTCTTGGCTTTGAGC	2186		
Db	261	GCAGGACTGTGGGCCCCCAACCCCTGCACAGCCCTCATCCCTCTTGGCTTTGAGC	202		
QY	2187	CGTCAGAGCCCTGTGCTCAGTGTCTGACCGAGACACTCACAGCTTTGTTCATCAGGGCAC	2246		
Db	201	CGTCAGAGCCCTGTGCTCAGTGTCTGACCGAGACACTCACAGCTTTGTTCATCAGGGCAC	142		
QY	2247	AGGCTTCTTCGAGCCAGGATGATCTGTGCCACGCTTGACCTCGGGCCCATCTGGGCTC	2306		
Db	141	AGGCTTCTTCGAGCCAGGATGATCTGTGCCACGCTTGACCTCGGGCCCATCTGGGCTC	82		
QY	2307	ATGCTCTCTCTCTGATTGAAATTAGTACCTAGCTGCACAGATGTAGTTACCAAAA	2366		

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c 67	63.6	2.7	205429	2	AC005506	AC005506 Plasmodium	c 140	39.6	1.7	167218	2	AC069041	AC069041 Homo sapi
c 68	63.6	2.7	251332	3	AE014846	AE014846 Plasmodium	c 141	39.6	1.7	179028	2	AC027046	AC027046 Homo sapi
c 69	63	2.6	3569	3	BT009934	BT009934 Drosophila	c 142	39.6	1.7	228436	2	AC113100	AC113100 Mus muscu
c 70	62.2	2.6	35030	8	SPBC27B12	AL021766 S. pombe c	c 143	39.4	1.6	2049	9	AK027165	AK027165 Homo sapi
c 71	62.2	2.6	38000	8	AB004539	AB004539 Schizosac	c 144	39.4	1.6	34631	9	AP001115	AP001115 Homo sapi
c 72	58.8	2.5	125020	9	AF429315	AF429315 Homo sapi	c 145	39.4	1.6	39875	9	AP001117	AP001117 Homo sapi
c 73	58.6	2.4	5448	9	AK074064	AK074064 Homo sapi	c 146	39.4	1.6	153441	9	BS000071	BS000071 Pan trogl
c 74	53	2.2	578	6	AR412615	AR412615 Sequence	c 147	39.4	1.6	177622	9	AC023559	AC023559 Homo sapi
c 75	53	2.2	578	6	BD108168	BD108168 EST and e	c 148	39.4	1.6	180571	9	AC113425	AC113425 Homo sapi
c 76	52.4	2.2	1894	9	BC013987	BC013987 Homo sapi	c 149	39.4	1.6	340000	9	HS21C027	HS21C027 Homo sapi
c 77	51	2.1	86765	9	AC004472	AC004472 Homo sapi	c 150	39.2	1.6	46996	9	AC112645	AC112645 Homo sapi
c 78	51	2.1	195102	9	AL353795	AL353795 Human DNA	c 151	39.2	1.6	99960	9	AC104637	AC104637 Homo sapi
c 79	51	2.1	198829	2	AL391668	AL391668 Homo sapi	c 152	39.2	1.6	187295	9	AC021531	AC021531 Homo sapi
c 80	49.2	2.1	3000	6	AX655393	AX655393 Sequence	c 153	39	1.6	2766	9	AK125744	AK125744 Homo sapi
c 81	48	2.0	125020	9	AF429315	AF429315 Homo sapi	c 154	39	1.6	132254	3	AC116330	AC116330 Dictyoste
c 82	46.2	1.9	2000	6	AX655393	AX655393 Sequence	c 155	39	1.6	160770	2	AC016796	AC016796 Homo sapi
c 83	45.6	1.9	3608	8	SCYL031C	W73136 S. cerevisia	c 156	39	1.6	170262	9	AC105398	AC105398 Homo sapi
c 84	44.8	1.9	786	11	CNS06KAV	AL402437 T3 end of	c 157	39	1.6	190651	9	AL353811	AL353811 Human DNA
c 85	44.4	1.9	1838	9	BC001030	BC001030 Homo sapi	c 158	38.8	1.6	832	6	AR415176	AR415176 Sequence
c 86	44.4	1.9	3048	6	AX488862	AX488862 Sequence	c 159	38.8	1.6	832	6	BD110729	BD110729 EST and e
c 87	43	1.8	124230	10	AC005259	AC005259 Mouse BAC	c 160	38.8	1.6	3492	6	AX226561	AX226561 Sequence
c 88	43	1.8	180424	9	AC106860	AC106860 Homo sapi	c 161	38.8	1.6	3493	6	AX226562	AX226562 Sequence
c 89	43	1.8	208030	10	AL672276	AL672276 Mouse DNA	c 162	38.8	1.6	9087	6	AX223857	AX223857 Sequence
c 90	42.2	1.8	186160	10	AC117213	AC117213 Mus muscu	c 163	38.8	1.6	9087	6	AX226507	AX226507 Sequence
c 91	42.2	1.8	231684	2	AC133955	AC133955 Mus muscu	c 164	38.8	1.6	11389	6	AX549158	AX549158 Sequence
c 92	42	1.8	7218	6	166494	166494 Sequence 14	c 165	38.8	1.6	11389	9	AF231024	AF231024 Homo sapi
c 93	41.8	1.7	142533	2	AC138160	AC138160 Rattus no	c 166	38.8	1.6	94516	8	AP004526	AP004526 Lotus cor
c 94	41.8	1.7	195988	2	AC141493	AC141493 Rattus no	c 167	38.8	1.6	111739	9	AF165424	AF165424 Homo sapi
c 95	41.8	1.7	276193	2	AC094506	AC094506 Rattus no	c 168	38.8	1.6	112655	9	AC103760	AC103760 Homo sapi
c 96	41.8	1.7	306781	2	AC119382	AC119382 Rattus no	c 169	38.8	1.6	120206	9	HS439F8	HS439F8 Human DNA
c 97	41.6	1.7	235236	5	AL954130	AL954130 Zebrafish	c 170	38.8	1.6	132843	9	AC083845	AC083845 Homo sapi
c 98	41	1.7	145575	2	AC135571	AC135571 Rattus no	c 171	38.8	1.6	142477	2	BX321989	BX321989 Danio rer
c 99	41	1.7	152306	2	AC117759	AC117759 Mus muscu	c 172	38.8	1.6	163460	2	AC069378	AC069378 Homo sapi
c 100	41	1.7	153890	2	AC092525	AC092525 Papio anu	c 173	38.8	1.6	166039	2	AC044855	AC044855 Homo sapi
c 101	41	1.7	161194	2	AC021466	AC021466 Homo sapi	c 174	38.8	1.6	191786	2	AC137533	AC137533 Bos tauru
c 102	41	1.7	165110	2	AC121317	AC121317 Mus muscu	c 175	38.8	1.6	215911	10	AC126957	AC126957 Rattus no
c 103	41	1.7	215985	2	AC137029	AC137029 Rattus no	c 176	38.8	1.6	229806	2	AC146954	AC146954 Otolenur
c 104	41	1.7	231268	2	AC118318	AC118318 Rattus no	c 177	38.8	1.6	250932	2	AC097598	AC097598 Rattus no
c 105	41	1.7	240453	2	AC103204	AC103204 Rattus no	c 178	38.8	1.6	308826	2	AC118525	AC118525 Rattus no
c 106	41	1.7	241998	2	AC112739	AC112739 Rattus no	c 179	38.8	1.6	347050	3	PPA929351	PPA929351 Plasmodiu
c 107	41	1.7	249846	2	AC117758	AC117758 Mus muscu	c 180	38.6	1.6	93754	2	AC138764	AC138764 Homo sapi
c 108	40.8	1.7	134971	2	AC116367	AC116367 Oryza sat	c 181	38.6	1.6	162503	9	AL357772	AL357772 Human DNA
c 109	40.6	1.7	839	11	BV017453	BV017453 S212P6014	c 182	38.6	1.6	179173	10	AL669973	AL669973 Mouse DNA
c 110	40.4	1.7	76485	3	AC024211	AC024211 Caenorhab	c 183	38.6	1.6	213109	2	AC134199	AC134199 Rattus no
c 111	40.4	1.7	76485	3	AC024872	AC024872 Caenorhab	c 184	38.6	1.6	252459	2	AC094717	AC094717 Rattus no
c 112	40.4	1.7	108865	9	HS034584	AL132661 Human DNA	c 185	38.4	1.6	31043	1	AY268081	AY268081 Candidatu
c 113	40.4	1.7	115393	8	AC091247	AC091247 Oryza sat	c 186	38.4	1.6	109477	9	AC104042	AC104042 Homo sapi
c 114	40.4	1.7	117505	8	AC096687	AC096687 Oryza sat	c 187	38.4	1.6	110779	9	BX470173	BX470173 Human DNA
c 115	40.4	1.7	140661	2	AC012425	AC012425 Homo sapi	c 188	38.4	1.6	117780	8	AP003988	AP003988 Oryza sat
c 116	40.4	1.7	145268	2	AC119340	AC119340 Rattus no	c 189	38.4	1.6	164798	9	AC092598	AC092598 Homo sapi
c 117	40.2	1.7	43543	6	AX711964	AX711964 Sequence	c 190	38.4	1.6	190325	9	AL732327	AL732327 Human DNA
c 118	40.2	1.7	92179	9	AL390965	AL390965 Human DNA	c 191	38.4	1.6	289967	2	EX511031	EX511031 Danio rer
c 119	40.2	1.7	163595	9	AC022076	AC022076 Homo sapi	c 192	38.2	1.6	2473	9	BC027955	BC027955 Homo sapi
c 120	40.2	1.7	180465	9	AC074011	AC074011 Homo sapi	c 193	38.2	1.6	131144	10	AL645569	AL645569 Mouse DNA
c 121	40.2	1.7	222088	2	AC079216	AC079216 Mus muscu	c 194	38.2	1.6	160794	2	AC124751	AC124751 Mus muscu
c 122	40.2	1.7	260668	2	AC069469	AC069469 Mus muscu	c 195	38	1.6	38	6	AX055482	AX055482 Sequence
c 123	40	1.7	5561	6	AX781118	AX781118 Sequence	c 196	38	1.6	60583	8	AB011475	AB011475 Arabidops
c 124	40	1.7	5561	6	AX780230	AX780230 Sequence	c 197	38	1.6	134971	2	AC116367	AC116367 Oryza sat
c 125	40	1.7	5745	9	AX405586	AX405586 Sequence	c 198	38	1.6	179163	2	AC117985	AC117985 Papio anu
c 126	40	1.7	6237	9	AB011117	AB011117 Homo sapi	c 199	38	1.6	180715	2	AC116932	AC116932 Papio anu
c 127	40	1.7	173119	9	AC079073	AC079073 Homo sapi	c 200	38	1.6	184582	9	AC010207	AC010207 Homo sapi
c 128	40	1.7	174670	2	AC068281	AC068281 Homo sapi	c 201	38	1.6	195138	2	AC118118	AC118118 Rattus no
c 129	40	1.7	188972	2	AC006907	AC006907 Caenorhab	c 202	38	1.6	235583	2	AC105659	AC105659 Rattus no
c 130	40	1.7	256744	2	AC132718	AC132718 Rattus no	c 203	37.8	1.6	110191	9	AC003001	AC003001 Homo sapi
c 131	40	1.7	282895	2	AC096056	AC096056 Rattus no	c 204	37.8	1.6	110000	2	LMFLCHR12_06	Continuation (7 of
c 132	39.8	1.7	120185	8	ATC07138	ATC07138 Arabidops	c 205	37.8	1.6	112646	9	AC010240	AC010240 Homo sapi
c 133	39.8	1.7	198220	8	ATC07138	ATC07138 Arabidops	c 206	37.8	1.6	137132	9	AC136628	AC136628 Homo sapi
c 134	39.8	1.7	198697	8	ATC07138	ATC07138 Arabidops	c 207	37.8	1.6	153650	9	AC022296	AC022296 Homo sapi
c 135	39.8	1.7	232443	2	AC099251	AC099251 Rattus no	c 208	37.8	1.6	155304	9	AC055845	AC055845 Homo sapi
c 136	39.8	1.7	266295	2	AC103500	AC103500 Rattus no	c 209	37.8	1.6	157088	10	AC127292	AC127292 Homo sapi
c 137	39.6	1.7	958	11	CNS06JEX	AL401503 T3 end of	c 210	37.8	1.6	167446	2	AC137718	AC137718 Homo sapi
c 138	39.6	1.7	7218	6	166494	166494 Sequence 14	c 211	37.8	1.6	177669	9	CNS05TE7	AC1358336 Human chr

C 212	37.8	1.6	179940	2	AC144813	AC144813 Mus muscu
C 213	37.8	1.6	180336	2	AC021731	AC021731 Homo sapi
C 214	37.8	1.6	180785	2	AC123979	AC123979 Papio anu
C 215	37.8	1.6	183902	2	AP003403	AP003403 Homo sapi
C 216	37.8	1.6	185953	2	AC136593	AC136593 Homo sapi
C 217	37.8	1.6	191603	2	AC110561	AC110561 Mus muscu
C 218	37.8	1.6	195843	2	AC023944	AC023944 Homo sapi
C 219	37.8	1.6	200675	2	AP004244	AP004244 Homo sapi
C 220	37.8	1.6	207298	2	AC136631	AC136631 Homo sapi
C 221	37.8	1.6	208472	10	AL833799	AL833799 Mouse DNA
C 222	37.8	1.6	220632	2	AC136596	AC136596 Homo sapi
C 223	37.8	1.6	37100	9	HS566H6	AL031845 Human DNA
C 224	37.6	1.6	98261	9	HS1054C24	AL035249 Human DNA
C 225	37.6	1.6	128683	2	AC135793	AC135793 Oryza sat
C 226	37.6	1.6	160545	9	AC036214	AC036214 Homo sapi
C 227	37.6	1.6	174347	10	AL928956	AL928956 Mouse DNA
C 228	37.6	1.6	180535	2	AC018952	AC018952 Homo sapi
C 229	37.6	1.6	196083	2	AC027092	AC027092 Homo sapi
C 230	37.4	1.6	446	6	AX676916	AX676916 Secreted
C 231	37.4	1.6	603	6	BD072152	BD072152 Secreted
C 232	37.4	1.6	2380	9	HS080848	BS648500 Homo sapi
C 233	37.4	1.6	2403	9	BT066637	BT066637 Homo sapi
C 234	37.4	1.6	2421	9	HSARAI	YL4314 Homo sapien
C 235	37.4	1.6	2460	6	AX099535	AX099535 Sequence
C 236	37.4	1.6	2460	6	BD190805	BD190805 Secreted
C 237	37.4	1.6	2506	9	AB006198	AB006198 Homo sapi
C 238	37.4	1.6	2526	9	BC001058	BC001058 Homo sapi
C 239	37.4	1.6	2527	6	AR309144	AR309144 Sequence
C 240	37.4	1.6	2527	9	AF353625	AF353625 Homo sapi
C 241	37.4	1.6	2550	6	AX078301	AX078301 Sequence
C 242	37.4	1.6	5637	6	AK126983	AK126983 Homo sapi
C 243	37.4	1.6	37286	2	LMF16852	AL034359 Leishmani
C 244	37.4	1.6	141819	5	AL935063	AL935063 Zebrafish
C 245	37.4	1.6	152468	2	AP001584	AP001584 Homo sapi
C 246	37.4	1.6	162328	9	AP000350	AP000350 Homo sapi
C 247	37.4	1.6	164840	2	AC011127	AC011127 Homo sapi
C 248	37.4	1.6	169553	9	AC022046	AC022046 Homo sapi
C 249	37.4	1.6	185782	9	AC074389	AC074389 Homo sapi
C 250	37.4	1.6	221926	2	EX005245	EX005245 Danio rer
C 251	37.4	1.6	247462	3	LMF10448	AL013974 Leishmani
C 252	37.4	1.6	252632	3	AE014818	AE014818 Plasmodiu
C 253	37.4	1.6	348077	1	AP003000	AP003000 Mesorhizo
C 254	37.2	1.6	4947	8	AF014927	AF014927 Chlamydom
C 255	37.2	1.6	9810	6	BD129571	BD129571 Polynucle
C 256	37.2	1.6	115499	2	AC130963	AC130963 Medicago
C 257	37.2	1.6	128590	2	AC009557	AC009557 Homo sapi
C 258	37.2	1.6	168448	9	AC009469	AC009469 Homo sapi
C 259	37.2	1.6	180189	5	EX005354	EX005354 Zebrafish
C 260	37.2	1.6	195848	10	AC117600	AC117600 Mus muscu
C 261	37.2	1.5	505	6	AR424142	AR424142 Sequence
C 262	37	1.5	505	6	BD119695	BD119695 EST and e
C 263	37	1.5	102477	9	AC008935	AC008935 Homo sapi
C 264	37	1.5	110000	2	AC120578	AC120578 Rattus no
C 265	37	1.5	110000	2	AC120578	Continuation (2 of
C 266	37	1.5	111990	9	AL360294	AL360294 Human DNA
C 267	37	1.5	123530	2	AL356369	AL356369 Homo sapi
C 268	37	1.5	161511	2	AC128773	AC128773 Rattus no
C 269	37	1.5	166357	9	AC091559	AC091559 Homo sapi
C 270	37	1.5	169862	2	AC025530	AC025530 Homo sapi
C 271	37	1.5	170358	9	AC008873	AC008873 Homo sapi
C 272	37	1.5	172138	2	AC064796	AC064796 Homo sapi
C 273	37	1.5	177797	2	AC016581	AC016581 Homo sapi
C 274	37	1.5	182829	10	AL627214	AL627214 Mouse DNA
C 275	37	1.5	183246	2	AC118486	AC118486 Rattus no
C 276	37	1.5	183389	2	AC110168	AC110168 Mus muscu
C 277	37	1.5	184118	9	AC016580	AC016580 Homo sapi
C 278	37	1.5	188559	2	AC124602	AC124602 Mus muscu
C 279	37	1.5	194965	2	AC121018	AC121018 Rattus no
C 280	37	1.5	208497	2	AC127844	AC127844 Rattus no
C 281	37	1.5	211431	2	AC111594	AC111594 Rattus no
C 282	37	1.5	217726	10	AL928680	AL928680 Mouse DNA
C 283	37	1.5	221805	10	AC105515	AC105515 Rattus no
C 284	37	1.5	221805	10	AC105515	
C 285	37	1.5	229276	2	AC120704	AC120704 Rattus no
C 286	37	1.5	236974	2	AC095207	AC095207 Rattus no
C 287	37	1.5	240833	2	AC107087	AC107087 Rattus no
C 288	37	1.5	251039	2	AL592290	AL592290 Homo sapi
C 289	37	1.5	255459	2	AC127743	AC127743 Rattus no
C 290	36.8	1.5	955	1	WFU74476	U74476 Wolbachia p
C 291	36.8	1.5	969	6	AR386073	AR386073 Sequence
C 292	36.8	1.5	992	8	AF325124	AF325124 Arabidops
C 293	36.8	1.5	1033	6	AR342189	AR342189 Sequence
C 294	36.8	1.5	1033	6	AX358283	AX358283 Sequence
C 295	36.8	1.5	1033	6	AF062915	AF062915 Arabidops
C 296	36.8	1.5	5399	10	ENMG7G	X07833 Rat glycine
C 297	36.8	1.5	85702	8	AC020665	AC020665 Arabidops
C 298	36.8	1.5	95169	8	AP006084	AP006084 Lotus cor
C 299	36.8	1.5	101739	9	AL591400	AL591400 Human DNA
C 300	36.8	1.5	124659	9	AL583828	AL583828 Human DNA
C 301	36.8	1.5	137312	2	AC141039	AC141039 Rattus no
C 302	36.8	1.5	141114	2	AC108903	AC108903 Felis cat
C 303	36.8	1.5	141186	2	AC015578	AC015578 Homo sapi
C 304	36.8	1.5	148452	2	AL954696	AL954696 Danio rer
C 305	36.8	1.5	153108	9	AL355273	AL355273 Human DNA
C 306	36.8	1.5	158745	9	AL136456	AL136456 Human DNA
C 307	36.8	1.5	161474	9	AL589791	AL589791 Human DNA
C 308	36.8	1.5	163198	2	AL161634	AL161634 Homo sapi
C 309	36.8	1.5	165570	2	AC015765	AC015765 Homo sapi
C 310	36.8	1.5	166207	9	AL135785	AL135785 Human DNA
C 311	36.8	1.5	167024	2	EX571816	EX571816 Homo sapi
C 312	36.8	1.5	178193	2	AC068949	AC068949 Homo sapi
C 313	36.8	1.5	178412	10	AL603864	AL603864 Mouse DNA
C 314	36.8	1.5	184463	10	AC126553	AC126553 Mus muscu
C 315	36.8	1.5	185560	2	AC129046	AC129046 Rattus no
C 316	36.8	1.5	194290	2	AC137228	AC137228 Rattus no
C 317	36.8	1.5	194317	2	AC137232	AC137232 Rattus no
C 318	36.8	1.5	197626	10	AC115117	AC115117 Mus muscu
C 319	36.8	1.5	216747	2	AC120299	AC120299 Rattus no
C 320	36.8	1.5	240477	2	AC117921	AC117921 Rattus no
C 321	36.8	1.5	256944	2	AC096512	AC096512 Rattus no
C 322	36.8	1.5	267649	2	AC128452	AC128452 Rattus no
C 323	36.6	1.5	279	9	HS4230319	HS4230319 Homo sapi
C 324	36.6	1.5	364	6	AR425705	AR425705 Sequence
C 325	36.6	1.5	364	6	BD121258	BD121258 EST and e
C 326	36.6	1.5	408	6	AX300942	AX300942 Sequence
C 327	36.6	1.5	2480	6	HUMGP1BA	AR380551 Sequence
C 328	36.6	1.5	2480	6	HUMGP1BA	J02940 Human plate
C 329	36.6	1.5	2923	6	BD234219	BD234219 ATP-bind
C 330	36.6	1.5	2923	6	BD234241	BD234241 ATP-bind
C 331	36.6	1.5	6062	9	HUMGP1BAA	M22403 Human blood
C 332	36.6	1.5	6241	9	AF395009	AF395009 Homo sapi
C 333	36.6	1.5	54353	1	AY210783	AY210783 Nodularia
C 334	36.6	1.5	80765	9	AC004009	AC004009 Homo sapi
C 335	36.6	1.5	91927	9	AC004771	AC004771 Homo sapi
C 336	36.6	1.5	94959	2	AC136765	AC136765 Homo sapi
C 337	36.6	1.5	110255	8	AC144514	AC144514 Medicago
C 338	36.6	1.5	110257	8	AC144609	AC144609 Medicago
C 339	36.6	1.5	114945	8	AC135467	AC135467 Medicago
C 340	36.6	1.5	123209	8	ATF4F15	AL049711 Arabidops
C 341	36.6	1.5	124394	9	AC087593	AC087593 Homo sapi
C 342	36.6	1.5	129169	2	AC032038	AC032038 Homo sapi
C 343	36.6	1.5	149850	9	AP001622	AP001622 Homo sapi
C 344	36.6	1.5	150074	2	AC016007	AC016007 Homo sapi
C 345	36.6	1.5	152651	2	AC015556	AC015556 Homo sapi
C 346	36.6	1.5	157075	9	AC005486	AC005486 Homo sapi
C 347	36.6	1.5	161083	2	AC129224	AC129224 Oryza sat
C 348	36.6	1.5	167865	2	AC053471	AC053471 Homo sapi
C 349	36.6	1.5	181511	9	AC015555	AC015555 Homo sapi
C 350	36.6	1.5	181825	9	AC109333	AC109333 Homo sapi
C 351	36.6	1.5	184595	2	AC015913	AC015913 Homo sapi
C 352	36.6	1.5	192000	1	AE001438	AE001438 Clostridi
C 353	36.6	1.5	198200	2	AC140668	AC140668 Canis fam
C 354	36.6	1.5	205050	1	AL646082	AL646082 Ralstonia
C 355	36.6	1.5	212199	9	AL445199	AL445199 Human DNA
C 356	36.6	1.5	213047	2	AC020557	AC020557 Homo sapi
C 357	36.6	1.5	221787	2	AC119782	AC119782 Rattus no

C 358	1.5	244451	2	AC125765	AC125765 Rattus no	431	36	1.5	1830	9	AY358622	Homo sapi
C 359	36.6	281000	3	TBCHRI12	AL929604 Trypanoso	432	36	1.5	1877	9	AY358622	Homo sapi
C 360	36.6	301439	1	AC015943	AL929604 Clostridi	433	36	1.5	1877	9	AY358622	Homo sapi
C 361	36.6	340000	9	AP001746	AP001746 Homo sapi	434	36	1.5	2039	9	AK126250	Homo sapi
C 362	36.6	348178	1	BX572092	BX572092 Prochlo	435	36	1.5	4088	9	AK128869	Homo sapi
C 363	36.4	714	6	AX763031	AX763031 Sequence	436	36	1.5	4494	9	AK024476	Homo sapi
C 364	36.4	2342	1	RU55213	U55213 Rickettsia	437	36	1.5	25815	9	HS321102	Human DNA
C 365	36.4	3325	5	AF117612	AF117612 Gallus ga	438	36	1.5	37144	2	BX293534	Danio rer
C 366	36.4	150502	1	AL014645	AL014645 Bifidobac	439	36	1.5	64674	9	AC087057	Homo sapi
C 367	36.4	65748	9	AL445666	AL445666 Human DNA	440	36	1.5	71166	2	AC023783	Homo sapi
C 368	36.4	1510395	2	AC096695	AC096695 Rattus no	441	36	1.5	95579	9	AC023162	Homo sapi
C 369	36.4	15123379	2	AC119409	AC119409 Medicago	442	36	1.5	98356	9	HS344J2	Homo sapi
C 370	36.4	15123672	2	AC121246	AC121246 Zebraphish	443	36	1.5	110000	2	BX649565	2
C 371	36.4	15150021	5	BX088691	BX088691 Zebraphish	444	36	1.5	110000	2	AC116957	0
C 372	36.4	15158716	2	AC102318	AC102318 Mus muscu	445	36	1.5	112058	9	AC055112	Homo sapi
C 373	36.4	15160434	2	AC018590	AC018590 Homo sapi	446	36	1.5	126083	9	AC105337	Homo sapi
C 374	36.4	15166748	2	AC115533	AC115533 Papio anu	447	36	1.5	135153	9	AL353605	Human DNA
C 375	36.4	15169283	2	AC044820	AC044820 Homo sapi	448	36	1.5	148008	2	AC092004	Bos tauru
C 376	36.4	15169510	2	AC130006	AC130006 Rattus no	449	36	1.5	149471	2	AP005921	Oryza sat
C 377	36.4	15184296	9	AC099047	AC099047 Homo sapi	450	36	1.5	154485	2	AC116894	Mus muscu
C 378	36.4	15187024	2	AC102093	AC102093 Mus muscu	451	36	1.5	154616	2	AC067772	Homo sapi
C 379	36.4	15121238	2	AC134077	AC134077 Rattus no	452	36	1.5	155770	2	AC092381	Homo sapi
C 380	36.4	151219457	2	AC095833	AC095833 Rattus no	453	36	1.5	1559082	2	AC025947	Homo sapi
C 381	36.4	151220710	2	AC125304	AC125304 Rattus no	454	36	1.5	164396	2	HSAC000380	Homo sapi
C 382	36.4	151231986	2	AC097904	AC097904 Rattus no	455	36	1.5	170935	2	AC092008	Bos tauru
C 383	36.4	151234639	2	AC145118	AC145118 Rattus no	456	36	1.5	172332	2	AC117167	Rattus no
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ALIGNMENTS

RESULT 1
 AX055478 2395 bp DNA linear PAT 13-JAN-2001
 LOCUS Sequence 108 from Patent WO073452.
 DEFINITION AX055478
 ACCESSION AX055478
 VERSION AX055478.1 GI:12228736
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J., Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L., Tumas, D., Watanabe, C.K. and Wood, W.I.
 TITLE Compositions and methods for the treatment of immune related diseases
 JOURNAL Patent: WO 0073452-A 108 07-DEC-2000;
 FEATURES Genentech, Inc. (US)
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 Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 3
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 LOCUS AX092408
 DEFINITION Sequence 139 from Patent WO0116318.
 ACCESSION AX092408
 VERSION AX092408.1 GI:13444518
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Baton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
 Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
 Wood,W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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 JOURNAL Patent: WO 0116318-A 139 08-MAR-2001;
 Genentech, Inc. (US)
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ORIGIN
 Query Match 100.0%; Score 2395; DB 6; Length 2395;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
Baker, K.P., Desnovers L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K., and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 117 13-DEC-2001;
Genentech Inc. (US)
FEATURES Location/Qualifiers
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Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis

JOURNAL Patent: WO 020690-A 291 03-JAN-2002;
Genentech, Inc. (US)

FEATURES Location/Qualifiers

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Xie,M.H., Yaneura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secretered Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL 12975309
PUBMED 2 (bases 1 to 2395)
REFERENCE Clark,H.F.
AUTHORS Direct Submission
TITLE Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
inc., 1 DNA Way, South San Francisco, CA 94080, USA
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue procurement: Lou Staudt
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@hgrl.nih.gov
 Akhtar, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lari, P., Legaspi, R., McDowell, J., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., Pearson, R., Stantirip, S., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Place: 93 Row: n Column: 15
 This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction.

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Tanechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuno,Y.
TITLE
JOURNAL
Patent: EP 1347046-A 1769 24-SEP-2003;
Research Association for Biotechnology (JP)
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COMMENT
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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Kanehori,K., Ishibaashi,T., Chiba,Y., Fujimori,K., Hiraoka,S.,
Tanai,H., Watanabe,S., Ishida,S., Ono,Y., Hotuta,T., Watanabe,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A.,
Ishii,S., Yamamoto,K., Isono,Y., Kawai-Hio,Y., Saito,K.,
Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A., Oshima,A.,
Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K.,
Masuko,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 2630)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamata, Kiseazu, Chiba 292-0812, Japan
(E-mail:genomics@kiseazu.co.jp, Tel.81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
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Evaluation; clone selection for full insert sequencing: HRI and
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Query Match 71.8%; Score 1719.4; DB 9; Length 2630;
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Fri Aug 6 10:49:39 2004

Db 2571 GTACCTAGCTGCAGCAGTATAGTATTACCAAGAAATAAACCGCAATAATTGAG 2625

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BD127295

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BD127295

Primer for synthesizing full-length cDNA and use thereof.

BD127295.1

GI:23222240

JP 2002017375-A/2726.

Homo sapiens (human)

Os

Homo sapiens (human)

PN JP 2002017375-A/2726

PD 22-JAN-2002

PF 07-JUL-2000 JP 2000253172

PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO

PI ISHII, YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI

SHINICHI KOJIMA,

PI TETSUJI OTSUKI, HISASHI KOGA

PC

Cl2N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC

10,

PC Cl2N21/02, C12N1/08, G06F17/30, C12N15/00, C12N5/00 CC

Primer for synthesizing full-length cDNA and use thereof FH Key

Location/Qualifiers

(116)..(3040).

FT CDS Location/Qualifiers

1..3197

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Best Local Similarity 98.4%; Pred. No. 0;

Matches 1555; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

QY 1 CTTGAGCGGAAAGCGCGCTGCAGCAGCGCGAGGCTCCAGGTGGGTCCGGTCCGCATC 60

Db 38 CTTGAGCGGAAAGCGCGCTGCAGCAGCGCGAGGCTCCAGGTGGGTCCGGTCCGCATC 97

QY 61 CAGCTTAGCGTGCACGATGGCTGGCTCCGGGACTTCCTACCTGTTGCGTAGCG 120

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QY 121 ATCGAGTCTAGGATCGCGTCTTCCTTCGGGGATTCCTCCGGCTCCGGTCCGTTCC 180

Db 158 ATCGAGTCTAGGATCGCGTCTTCCTTCGGGGATTCCTCCGGCTCCGGTCCGTTCC 217

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QY 241 TCTAACTGGACCGCTGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGAGCGGAG 300

Db 278 TCTAACTGGACCGCTGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGAGCGGAG 337

QY 301 GCCTTGAGAGATGATTTTGTGTTTGGGTCAAAGGCTGTGAATTTATGCTTCTGATAGAT 360

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 VERSION AK074815.1 GI:22760509
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,
 Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Iehi, S.,
 Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y.,
 Kojima, S., Nagahara, K., Masuo, Y., Ono, T., Okano, K., Yoshikawa, Y.,
 Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
 Nimomiyu, K.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3197)

AUTHORS Isogai, T. and Otsuki, T.

TITLE Direct Submission

JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology; cDNA library construction:
 Institute of Medical Science, University of Tokyo, Laboratory of
 Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
 sequencing and clone selection: Helix Research Institute (supported
 by Japan Key Technology Center etc.).

FEATURES

source

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induction"

116..3043

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CDS

ORIGIN

Query Match 63.5%; Score 1521.2; DB 9; Length 3197;
 Best Local Similarity 98.4%; Pred. No. 0;
 Matches 1555; Conservative 0; Mismatches 3; Indels 22; Gaps 1;
 QY 1 CTGGAGCGGAGCGCGCTGCAGCAGCGCGAGGCTCCAGGTGGGGTTCGGTTCCGCATC 60
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 QY 61 CAGCCTAGCGTGTCCACGATGCGGCTCGGACTTTCCGTAACCTGTTGCGTAGCG 120
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SHINTCHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
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Primer for synthesizing full-length cDNA and use thereof PH Key
Location/Qualifiers
(176).. (2857).

FT CDS
Location/Qualifiers
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FEATURES
source

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Best Local Similarity 96.4%; Pred. No. 0;
Matches 1325; Conservative 0; Mismatches 4; Indels 46; Gaps 1;

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RESULT 14
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LOCUS
DEFINITION
Primer for synthesizing full-length cDNA and use thereof.
ACCESSION
BD127743
VERSION
BD127743.1 GI:23222688
KEYWORDS
JP 2002017375-A/3174.
SOURCE
Homo sapiens (human)
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Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,
Wakamatsu, A., Sugiyama, T., Negai, K., Kojima, S., Otsuki, T. and
Koga, H.
Primer for synthesizing full-length cDNA and use thereof
PATENT: JP 2002017375-A 3174 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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PN JP 2002017375-A/3174
PD 22-JAN-2002
PF 07-JUL-2000 JP 2002053172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI

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ACCESSION	AK074715		
VERSION	AK074715.1	GI:22760337	
KEYWORDS	oligo capping; fis (full insert sequence).		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahara, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuma, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.		
TITLE	NEDO human cDNA sequencing project		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3019)		
AUTHORS	Isogai, T. and Otsuki, T.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).		
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445	101.8	4.3	3671	15	US-10-188-767-265	Sequence 265, App							
446	101.8	4.3	3671	15	US-10-188-769-265	Sequence 265, App							
447	101.8	4.3	3671	15	US-10-188-770-265	Sequence 265, App							
448	101.8	4.3	3671	15	US-10-188-773-265	Sequence 265, App							
449	101.8	4.3	3671	15	US-10-188-781-265	Sequence 265, App							
450	101.8	4.3	3671	15	US-10-194-361-265	Sequence 265, App							
451	101.8	4.3	3671	15	US-10-194-423-265	Sequence 265, App							
452	101.8	4.3	3671	15	US-10-195-897-265	Sequence 265, App							

ALIGNMENTS

RESULT 1

US-09-931-836-44
; Sequence 44, Application US/09931836
; Publication No. US20030027249A1
; GENERAL INFORMATION:
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3030R1C1
; CURRENT APPLICATION NUMBER: US/09/931,836
; CURRENT FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
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; PRIOR APPLICATION NUMBER: 09/874503
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; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827

; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
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; PRIOR FILING DATE: 2000-06-02
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; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; SEQ ID NO 44
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-931-836-44

Query Match 100.0%; Score 2395; DB 10; Length 2395;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CCTGAGCCGGAAGCGGGCTGCAGCAGGCGGAGCTCCAGGTGGGTTCGGCATC 60

Qy 61 CAGCTAGCGTGTCCAGATCGGCTGGGCTCGGGACTTTCGCTACCTGTTGGTAGCG 120

Db 61 CAGCTAGCGTGTCCAGATCGGCTGGGCTCGGGACTTTCGCTACCTGTTGGTAGCG 120

Qy 121 ATCGAGGTGCTAGGATCGCGGTCTTCTTCGGGGATTCTTCCGGCTCCCGTTTCGTTCC 180

Db 121 ATCGAGGTGCTAGGATCGCGGTCTTCTTCGGGGATTCTTCCGGCTCCCGTTTCGTTCC 180

Qy 181 TCTGCCAGAGCGGAACACGAGCGGAGCCGCCAGCCGCGGAGCCCTCGGCTGGAGCCAGT 240

Db 181 TCTGCCAGAGCGGAACACGAGCGGAGCCGCCAGCCGCGGAGCCCTCGGCTGGAGCCAGT 240

Qy 241 TCTAACTGGACACGCTGCCACCACTCTCTTCAAGTAAGTTGTTATTTCTGATAGAT 300

Db 241 TCTAACTGGACACGCTGCCACCACTCTCTTCAAGTAAGTTGTTATTTCTGATAGAT 300

Qy 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGTGTGAATTTATCCCTTACACAACT 360

Db 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGTGTGAATTTATCCCTTACACAACT 360

Qy 361 TACCTTGTGGAAGGAGCATCTCAGATTTTGTGGCTGAAGCAAGCCACCTACAGTT 420

Db 361 TACCTTGTGGAAGGAGCATCTCAGATTTTGTGGCTGAAGCAAGCCACCTACAGTT 420

Qy 421 ACTATGCTCGAATCAAGGCATTTGATGACGGGGAGCCCTTCTCGCTTTGTTCGATCATC 480

Db	421	ACTATGCTCGAATCAAGGCAATGATGAGGGAGCCTCTCTGGCTTTGTGCACTCATC	480
Qy	481	AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAGCAGCT	540
Db	481	AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAGCAGCT	540
Qy	541	GGAAAAAGAAATAGTCTTTTATGAGATGAACCTGGTTAAATTTATTTCCCAAGCATTTT	600
Db	541	GGAAAAAGAAATAGTCTTTTATGAGATGAACCTGGTTAAATTTATTTCCCAAGCATTTT	600
Qy	601	GTGGGAATATGATGGAAACCACTCATTTTTCGTGTGATGATACACAGAGTGTGATAATAT	660
Db	601	GTGGGAATATGATGGAAACCACTCATTTTTCGTGTGATGATACACAGAGTGTGATAATAT	660
Qy	661	GTACGAGGCAATTTGGATAAGATTTAAAGAGAGATTTGGGACATATTAATCTCCAC	720
Db	661	GTACGAGGCAATTTGGATAAGATTTAAAGAGAGATTTGGGACATATTAATCTCCAC	720
Qy	721	TACCTGGGGCTGGACACATTTGGCCACATTTTTCAGGGCCCAACAGCCCTGATTTGGCAG	780
Db	721	TACCTGGGGCTGGACACATTTGGCCACATTTTTCAGGGCCCAACAGCCCTGATTTGGCAG	780
Qy	781	AACTGTAGCGAGATGACAGCGCTGTGATGAAGATCCACACCTCACTGCACTCGAAGGAG	840
Db	781	AACTGTAGCGAGATGACAGCGCTGTGATGAAGATCCACACCTCACTGCACTCGAAGGAG	840
Qy	841	AGAGAGACGCTTTACCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAACA	900
Db	841	AGAGAGACGCTTTACCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAACA	900
Qy	901	GGAACTCAGGGGCTCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAACTCAGTTCT	960
Db	901	GGAACTCAGGGGCTCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAACTCAGTTCT	960
Qy	961	GGCTTTGAAAGAAACCCCGTGATATCCGACATCCAAAGCAGCTCCAAATAGACGGATGTG	1020
Db	961	GGCTTTGAAAGAAACCCCGTGATATCCGACATCCAAAGCAGCTCCAAATAGACGGATGTG	1020
Qy	1021	GCTCGACACTGCGGATAGACATTTGGCTTACCGATTCGAAAGACAGTGTAGGAGCCTC	1080
Db	1021	GCTCGACACTGCGGATAGACATTTGGCTTACCGATTCGAAAGACAGTGTAGGAGCCTC	1080
Qy	1081	CTATTCCAGTTGTGAAAGAAACCAATGAGAGCGGTGAGATTTTACATTTGAAT	1140
Db	1081	CTATTCCAGTTGTGAAAGAAACCAATGAGAGCGGTGAGATTTTACATTTGAAT	1140
Qy	1141	ACAGTGCAGCTTAGTAAACTGTTGCAAGAAATGTGCGCTCATATGAAAAAGATCTCTGGG	1200
Db	1141	ACAGTGCAGCTTAGTAAACTGTTGCAAGAAATGTGCGCTCATATGAAAAAGATCTCTGGG	1200
Qy	1201	TTTGACAGTTTAAATGTGCAAGAAATGTGCAAGAAATGTGCGCTCATATGAAAAAGATCTCTGGG	1260
Db	1201	TTTGACAGTTTAAATGTGCAAGAAATGTGCAAGAAATGTGCGCTCATATGAAAAAGATCTCTGGG	1260
Qy	1261	GAAAGCATTGCAAGTCTTATTTCACTGGGCTCCAAAGTTCTCAGGCACTACCTGGAT	1320
Db	1261	GAAAGCATTGCAAGTCTTATTTCACTGGGCTCCAAAGTTCTCAGGCACTACCTGGAT	1320
Qy	1321	GCTCTGAAGACGCTGAGCTTTGCTCCCTGAGTGCAAGTGGCCCAAGTTCTCACCTGTCTCC	1380
Db	1321	GCTCTGAAGACGCTGAGCTTTGCTCCCTGAGTGCAAGTGGCCCAAGTTCTCACCTGTCTCC	1380
Qy	1381	TGCTCAGGCTCCACAGGCACTGACAGAAAGCTGAGCTGGAGTCCCACTGTCACTC	1440
Db	1381	TGCTCAGGCTCCACAGGCACTGACAGAAAGCTGAGCTGGAGTCCCACTGTCACTC	1440
Qy	1441	CTGGTTTCTCTGCTCTTTTATTTGATGATCTGTTCTTTTCGGCGGTTCACTGATG	1500
Db	1441	CTGGTTTCTCTGCTCTTTTATTTGATGATCTGTTCTTTTCGGCGGTTCACTGATG	1500
Qy	1501	TGTGCACTCAGCTGAAAGTTGTGCTATCTTGTGGCCTCTCTGTGGCTGGCGGAGCT	1560

Db	1501	TGTGCACTCAGCTGAAAGTTCTGTGCTACTTCTGTGGCTCTCTGTGGCTGGCGGAGGCT	1560
Qy	1561	GCCTTTCTTTTACAGACTCTGTTTGAACACCTGTGTGTGCAAGTGTCTGCACTGCCC	1620
Db	1561	GCCTTTCTTTTACAGACTCTGTTTGAACACCTGTGTGTGCAAGTGTCTGCACTGCCC	1620
Qy	1621	TGGAAGAGGGGCTCAGGGAAAGGACGTGGAGCAGCTTATCCCAAGCTCTGGGTGTCCC	1680
Db	1621	TGGAAGAGGGGCTCAGGGAAAGGACGTGGAGCAGCTTATCCCAAGCTCTGGGTGTCCC	1680
Qy	1681	GACAGAGTGTTCACATCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	1740
Db	1681	GACAGAGTGTTCACATCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	1740
Qy	1741	TCCTCGCACTGTGTACCAAGTGTATTAAGAGCTGGCGGTTCACAGAGGAAACAAGCCCC	1800
Db	1741	TCCTCGCACTGTGTACCAAGTGTATTAAGAGCTGGCGGTTCACAGAGGAAACAAGCCCC	1800
Qy	1801	CAGCTGAGGGGTGTGTGAATCGACAGCTCCAGAGAGGTGTGGAGCTGTGAGTGTGAGT	1860
Db	1801	CAGCTGAGGGGTGTGTGAATCGACAGCTCCAGAGAGGTGTGGAGCTGTGAGTGTGAGT	1860
Qy	1861	GGGAGAGAGACAAATCGGCTTGGACACTCAGAGGGGTCAAAAGAGACTTGTGTGCAAC	1920
Db	1861	GGGAGAGAGACAAATCGGCTTGGACACTCAGAGGGGTCAAAAGAGACTTGTGTGCAAC	1920
Qy	1921	ACTCATCTGCCACACCCCAAGAAATGATCTGTGCTCATCAGTCCAGATTTCTTTTCAAGG	1980
Db	1921	ACTCATCTGCCACACCCCAAGAAATGATCTGTGCTCATCAGTCCAGATTTCTTTTCAAGG	1980
Qy	1981	CGGAGTGTGTGTGGAATTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG	2040
Db	1981	CGGAGTGTGTGTGGAATTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG	2040
Qy	2041	GGAGTGTGTGTGAGCAGTGAAGAGGGCGGATGTGCTCAGTCCAGATCCACAGAGCCCA	2100
Db	2041	GGAGTGTGTGTGAGCAGTGAAGAGGGCGGATGTGCTCAGTCCAGATCCACAGAGCCCA	2100
Qy	2101	GGATCAAGGAGCCCACTGCACTGGCAGAGGAGTGTGGGCCCCCAACCCCTGCAAC	2160
Db	2101	GGATCAAGGAGCCCACTGCACTGGCAGAGGAGTGTGGGCCCCCAACCCCTGCAAC	2160
Qy	2161	AGCCCTCATCCCTCTTGGCTTGGAGCCCTCAGAGGCGCTGTGCTGAGTGTCTACCGAGA	2220
Db	2161	AGCCCTCATCCCTCTTGGCTTGGAGCCCTCAGAGGCGCTGTGCTGAGTGTCTACCGAGA	2220
Qy	2221	CACCTCAGCTTGTTCATCAGGSCACAGGCTTCTCGAGCCAGGATGATCTGTGCCACG	2280
Db	2221	CACCTCAGCTTGTTCATCAGGSCACAGGCTTCTCGAGCCAGGATGATCTGTGCCACG	2280
Qy	2281	CTTGCACTCTGGGCCCCCATCTGGGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2340
Db	2281	CTTGCACTCTGGGCCCCCATCTGGGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2340
Qy	2341	CTGCAACAGATGTAGTTTACCAAAAGATTAACGGCAATAATTTGAGAAAAAAA	2395
Db	2341	CTGCAACAGATGTAGTTTACCAAAAGATTAACGGCAATAATTTGAGAAAAAAA	2395

RESULT 2
US-10-081-056-291
; Sequence 291, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.

; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Ye, Weilan
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
 ; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
 ; FILE REFERENCE: P3235P1C1
 ; CURRENT APPLICATION NUMBER: US/10/081,056
 ; CURRENT FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: PCT/US01/21735
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: US 60/219,556
 ; PRIOR FILING DATE: 2000-07-20
 ; PRIOR APPLICATION NUMBER: US 60/220,624
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: US 60/220,664
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: US 60/222,695
 ; PRIOR FILING DATE: 2000-08-02
 ; PRIOR APPLICATION NUMBER: US 09/643,657
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: PCT/US00/23522
 ; PRIOR FILING DATE: 2000-08-23
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
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 ; PRIOR FILING DATE: 2000-09-07
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 ; PRIOR FILING DATE: 2000-12-20
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 ; PRIOR FILING DATE: 2001-01-22
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 ; PRIOR APPLICATION NUMBER: US 09/866,028

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 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/17800
 ; PRIOR FILING DATE: 2001-06-01
 ; PRIOR APPLICATION NUMBER: PCT/US01/19692
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: PCT/US01/00000
 ; PRIOR FILING DATE: 2001-06-28
 ; NUMBER OF SEQ ID NOS: 383
 ; SEQ ID NO 291
 ; LENGTH: 2395
 ; TYPE: DNA
 ; ORGANISM: Homosapiens
 ; US-10-081-056-291

Query Match 100.0%; Score 2395; DB 13; Length 2395;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CCTGAGCGGGAAGCGCGGCTGCACGAGCGGAGCTCCAGGTGGGTTCGGTTCGGCATC	60
Db	1	CCTGAGCGGGAAGCGCGGCTGCACGAGCGGAGCTCCAGGTGGGTTCGGTTCGGCATC	60
QY	61	CAGCCTAGCGTGTCCAGATCGGCTCGGAGCTTTTCGTTACCTGTTGCGTAGCG	120
Db	61	CAGCCTAGCGTGTCCAGATCGGCTCGGAGCTTTTCGTTACCTGTTGCGTAGCG	120
QY	121	ATCGAGGTCTAGGATCGCGGTCTTCTTCGGGATTTCTCCGGCTCCCGTTCGTTCC	180
Db	121	ATCGAGGTCTAGGATCGCGGTCTTCTTCGGGATTTCTCCGGCTCCCGTTCGTTCC	180
QY	181	TCTGCCAGAGCGGAACACGAGCGGAGCGCCCGAGCGCCGAAACCTTCGGCTGGAGCCAGT	240
Db	181	TCTGCCAGAGCGGAACACGAGCGGAGCGCCCGAGCGCCGAAACCTTCGGCTGGAGCCAGT	240
QY	241	TCTAACTGGACACGCTGCCACCTCTCTTCAGTAAAGTTGTTATTTCTGATAGAT	300
Db	241	TCTAACTGGACACGCTGCCACCTCTCTTCAGTAAAGTTGTTATTTCTGATAGAT	300
QY	301	GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGTTGTAATTTATGCGCTACACACT	360
Db	301	GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGTTGTAATTTATGCGCTACACACT	360
QY	361	TACCTTGTGGAAGGAGGACATCTCACAGTTTTCGTGCTGAAGCAAGCCACCTACAGTT	420
Db	361	TACCTTGTGGAAGGAGGACATCTCACAGTTTTCGTGCTGAAGCAAGCCACCTACAGTT	420
QY	421	ACTATGCTCGAATCAAGGCAATTCATGACGGGAGCTTCCTGCTTTGTCAGCTCATC	480
Db	421	ACTATGCTCGAATCAAGGCAATTCATGACGGGAGCTTCCTGCTTTGTCAGCTCATC	480
QY	481	AGGAACCTCAATTCCTCGCATCTGCGAGACAGTGTGATTAAGCAAGCAAGGAGCT	540
Db	481	AGGAACCTCAATTCCTCGCATCTGCGAGACAGTGTGATTAAGCAAGCAAGGAGCT	540
QY	541	GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTAAATTTATTTCCCAAGCATTTT	600
Db	541	GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTAAATTTATTTCCCAAGCATTTT	600
QY	601	GTGAATATGATGGAACAACTCTATTTTCGTGTCAGATTACACAGAGGTGATTAATAAT	660
Db	601	GTGAATATGATGGAACAACTCTATTTTCGTGTCAGATTACACAGAGGTGATTAATAAT	660
QY	661	GTACAGAGGATTTGGATTAAGTATTAAGAGGAGATTTGGGACATTAATCTCTCAC	720
Db	661	GTACAGAGGATTTGGATTAAGTATTAAGAGGAGATTTGGGACATTAATCTCTCAC	720


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; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 117
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-535-117

Query Match      100.0%; Score 2395; DB 13; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGAGCGGGAAGCGCGCTCAGCAGGGCGAGGCTCCAGGTGGGGTGGTTCGGCATC 60
DB 1 CCTGAGCGGGAAGCGCGCTCAGCAGGGCGAGGCTCCAGGTGGGGTGGTTCGGCATC 60

QY 61 CAGCCTAGCGTCTCCACGATGGCGTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCG 120
DB 61 CAGCCTAGCGTCTCCACGATGGCGTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCG 120

QY 121 ATCGAGGTGCTAGGATCGCGTCTTCTTCCGGGATTCCTCCGGCTCCGGTTCGTTCC 180
DB 121 ATCGAGGTGCTAGGATCGCGTCTTCTTCCGGGATTCCTCCGGCTCCGGTTCGTTCC 180

QY 181 TCTGCGAGCGGGAACAGGAGCGGAGCCCGCAGCGCCGACCCCTCGGCTGGAGCCAGT 240
DB 181 TCTGCGAGCGGGAACAGGAGCGGAGCCCGCAGCGCCGACCCCTCGGCTGGAGCCAGT 240

QY 241 TCTAATCGGACCGCTGCCACCACTCTCTCAGTAAAGTGTGTAATTTATGCTGATAGAT 300
DB 241 TCTAATCGGACCGCTGCCACCACTCTCTCAGTAAAGTGTGTAATTTATGCTGATAGAT 300

QY 301 GCCTTGAGAGATGATTTTGTGTGGGTCAAAGGTGTGAAATTTATGCGCTTACACAACT 360
DB 301 GCCTTGAGAGATGATTTTGTGTGGGTCAAAGGTGTGAAATTTATGCGCTTACACAACT 360

QY 361 TACCTTGTGGAAGAAAGAGCATCTCACAGTTTGTGGCTGAAGCAAGCAAGCACTACAGT 420
DB 361 TACCTTGTGGAAGAAAGAGCATCTCACAGTTTGTGGCTGAAGCAAGCAAGCACTACAGT 420

QY 421 ACTATGCTCGAATCAAGCGATGATGACGGGAGCCCTCTCGGCTTTGTGACGTCAATC 480
DB 421 ACTATGCTCGAATCAAGCGATGATGACGGGAGCCCTCTCGGCTTTGTGACGTCAATC 480

QY 481 AGGAACCTCAATTTCTCTGCACTGTGGAAGACAGTGTGTAAGCAAGCAAGCAAGCACT 540
DB 481 AGGAACCTCAATTTCTCTGCACTGTGGAAGACAGTGTGTAAGCAAGCAAGCAAGCACT 540

QY 541 GGAAGAAAGATAGCTTTTATGGAGATGAACCTGGGTTAAATTTATCCCAAGCATTTT 600
DB 541 GGAAGAAAGATAGCTTTTATGGAGATGAACCTGGGTTAAATTTATCCCAAGCATTTT 600

QY 601 GTGGAATATGATGGAACCAACTCTATTTTCTGTGTCAGATTACACAGAGTGGATAATAT 660
DB 601 GTGGAATATGATGGAACCAACTCTATTTTCTGTGTCAGATTACACAGAGTGGATAATAT 660

QY 661 GTCACGAGGCAATTTGGATAAGTATTAAGAGAGAGATTTGGGACATATTAATCTCCAC 720
DB 661 GTCACGAGGCAATTTGGATAAGTATTAAGAGAGAGATTTGGGACATATTAATCTCCAC 720

QY 721 TACCTGGGGCTGGACCAATTTGGGCAATTTTACGGGCCCAACAGCCCCCTGATTTGGGCG 780
DB 721 TACCTGGGGCTGGACCAATTTGGGCAATTTTACGGGCCCAACAGCCCCCTGATTTGGGCG 780

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QY 781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGAGTGAAGGAG 840
DB 781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGAGTGAAGGAG 840

QY 841 AGAGAGACGCTTTTACCCAAATTTGCTGGTCTTTTGTGGTACCATGGCATGTGAAACA 900
DB 841 AGAGAGACGCTTTTACCCAAATTTGCTGGTCTTTTGTGGTACCATGGCATGTGAAACA 900

QY 901 GGAAGTCACGGGCTCTCCACAGGAGGTGAATACACCTCTGATTTTAACTCACTTCT 960
DB 901 GGAAGTCACGGGCTCTCTCCACAGGAGGTGAATACACCTCTGATTTTAACTCACTTCT 960

QY 961 GCGTTTGAAGGAAACCCCGGTGATATCCGACATCAAAAGCACGTCCAAATAGACGGATG 1020
DB 961 GCGTTTGAAGGAAACCCCGGTGATATCCGACATCAAAAGCACGTCCAAATAGACGGATG 1020

QY 1021 GCTGCGACACTGGCGATAGACACTTGGCTTACCGATTCGATTCGATTCGATTCGATTC 1080
DB 1021 GCTGCGACACTGGCGATAGACACTTGGCTTACCGATTCGATTCGATTCGATTCGATTC 1080

QY 1081 CTATTTCCCAAGTTTGAAGGAAAGACCAATGAGAGAGCAGTTGAGATTTTATCATTTGAAT 1140
DB 1081 CTATTTCCCAAGTTTGAAGGAAAGACCAATGAGAGAGCAGTTGAGATTTTATCATTTGAAT 1140

QY 1141 ACAGTGCGAGCTTAGTAAACTGTTGCAAGAGAAATGTCGCTCATATGAAAGAGATCCTGGG 1200
DB 1141 ACAGTGCGAGCTTAGTAAACTGTTGCAAGAGAAATGTCGCTCATATGAAAGAGATCCTGGG 1200

QY 1201 TTTGAGCAGTTTAAATGTCAGAAAGATGCAATGGAACTGGATCAGACTGACTGTTGGAG 1260
DB 1201 TTTGAGCAGTTTAAATGTCAGAAAGATGCAATGGAACTGGATCAGACTGACTGTTGGAG 1260

QY 1261 GAAAGACATTCAGAAAGTCTATTTCAACCTGGCTCCAAAGTTCTCAGGAGTACCTGGAT 1320
DB 1261 GAAAGACATTCAGAAAGTCTATTTCAACCTGGCTCCAAAGTTCTCAGGAGTACCTGGAT 1320

QY 1321 GCTTGAAGACGCTGAGCTTGTCCCTGAGTGCAAGTGGCCAGTTCCTCACTGCTGCTCC 1380
DB 1321 GCTTGAAGACGCTGAGCTTGTCCCTGAGTGCAAGTGGCCAGTTCCTCACTGCTGCTCC 1380

QY 1381 TGCTCAGCGTCCCAAGGACCTGCAAGAGGCTGAGCTGGAAGTCCACATGCTCATCTC 1440
DB 1381 TGCTCAGCGTCCCAAGGACCTGCAAGAGGCTGAGCTGGAAGTCCACATGCTCATCTC 1440

QY 1441 CTGGGTTTTCTGCTCTTTTATTTGTTGATCTCTGTTCTTTTGGGCTTTCAGGCTCATG 1500
DB 1441 CTGGGTTTTCTGCTCTTTTATTTGTTGATCTCTGTTCTTTTGGGCTTTCAGGCTCATG 1500

QY 1501 TGTGACCTCAGCTGAAAGTTGCTGCTACTTCTGTGGCTCTGTGGCTGCGGAGGCT 1560
DB 1501 TGTGACCTCAGCTGAAAGTTGCTGCTACTTCTGTGGCTCTGTGGCTGCGGAGGCT 1560

QY 1561 GCCTTTCTGTTTACAGACTCTGTTGACACTGCTGTTGTCGCAAGTCTGCGAGTGCCTC 1620
DB 1561 GCCTTTCTGTTTACAGACTCTGTTGACACTGCTGTTGTCGCAAGTCTGCGAGTGCCTC 1620

QY 1621 TGGACAGGGGCTCAGGGAAGGACGTGGAGCAGCTTATCCAGGCTCTGCGGTGCTCC 1680
DB 1621 TGGACAGGGGCTCAGGGAAGGACGTGGAGCAGCTTATCCAGGCTCTGCGGTGCTCC 1680

QY 1681 GACACAGTGTTCACATCTGCTGCTGTCAGGTGATGCTCAGTTCCTGGAAGAGTAGT 1740
DB 1681 GACACAGTGTTCACATCTGCTGCTGTCAGGTGATGCTCAGTTCCTGGAAGAGTAGT 1740

QY 1741 TCCTGCGACTGTTTACCAAGGTGATTTAAAGAGTGGCGGTACAGAGGAAACAGCCCCC 1800
DB 1741 TCCTGCGACTGTTTACCAAGGTGATTTAAAGAGTGGCGGTACAGAGGAAACAGCCCCC 1800

QY 1801 CAGCTGAGGGGCTGTGTGAATCGGACAGCTCCAGCAGAGGTGTTGGAGCTGAGCTGA 1860
DB 1801 CAGCTGAGGGGCTGTGTGAATCGGACAGCTCCAGCAGAGGTGTTGGAGCTGAGCTGA 1860

QY 1861 GGGGAAGAGACAAATCGGCTGGACACTCAGGAGGGTCAAAAGGAGACTTGTGTCGACC 1920

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[illegible]

:	PRIOR APPLICATION NUMBER:	60/079656					
:	PRIOR FILING DATE:	1998-03-26					
:	PRIOR APPLICATION NUMBER:	60/079728					
:	PRIOR FILING DATE:	1998-03-27					
:	Remaining Prior Application data removed - See File Wrapper or PALM.						
:	NUMBER OF SEQ ID NOS:	246					
:	SEQ ID NO 117:						
:	LENGTH:	2395					
:	TYPE:	DNA					
:	ORGANISM:	Homo Sapien					
:	US-10-232-230-117						
<hr/>							
	Query Match	100.0%;	Score 2395;	DB 13;	Length 2395;		
	Best Local Similarity	100.0%;	Pred. No. 0;				
	Matches 2395;	Conservative	0;	Mismatches	0;	Indels	Gaps 0;
<hr/>							
QY	1	CCTGAGCGCGAAGCGGGCTGCACAGAGGCCAGGCTCCAGGTGGGTGGTTCGGCATC	60				
DB	1	CCTGAGCGCGAAGCGCGGCTCACAGCGGGCAGGCTCCAGGTGGGTGGTTCGGTTCGGCATC	60				
QY	61	CAGCCTAGCGTGCTCCACGATGCGGTGGGCTCCGGGACTTTCCGTACCTGTTCGGTAGCG	120				
DB	61	CAGCCTAGCGGTGTCCACGATGCGGTGGGCTCCGGGACTTTCCGTACCTGTTCGGTAGCG	120				
QY	121	ATCGAGGTGCTAGGATCCGCTTTCCTTCGGGGAATTCTTCCGGCTCCCGTTCGTTCC	180				
DB	121	ATCGAGGTGCTAGGATCCGCTTTCCTTCGGGGAATTCTTCCGGCTCCCGTTCGTTCC	180				
QY	181	TCTGCCAGCGCAACACGGAGGGAGCCCCCAGCGCCCAGAACCCCTCGCTGGAGCGCACT	240				
DB	181	TCTGCCAGCGCAACACGGAGGGAGCCCCCAGCGCCCAGAACCCCTCGCTGGAGCGCACT	240				
QY	241	TCTAACTGCACACGCTGCCACCACTCTCTTCAGTAAAGTTGTATTGTTCTGTATAGAT	300				
DB	241	TCTAACTGCACACGCTGCCACCACTCTCTTCAGTAAAGTTGTATTGTTCTGTATAGAT	300				
QY	301	GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGTTGTGAAATTAATGCCCTACACAAC	360				
DB	301	GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGTTGTGAAATTAATGCCCTACACAAC	360				
QY	361	TACCTTGTGMAAAGGAGCATCTCACAGTTTTGTGGCTGAAGCAAGCCACCCTACAGTT	420				
DB	361	TACCTTGTGMAAAGGAGCATCTCACAGTTTTGTGGCTGAAGCAAGCCACCCTACAGTT	420				
QY	421	ACTATGCTCGAATCAAGGATTTGATGACGGGAGCGCTTCCTGGCTTGTTCGACGTCATC	480				
DB	421	ACTATGCTCGAATCAAGGATTTGATGACGGGAGCGCTTCCTGGCTTGTTCGACGTCATC	480				
QY	481	AGGAACCTCAATTTCTCTGCACCTGCTGGAAGACAGTGTGATAAGAAGCAAGAGCAGCT	540				
DB	481	AGGAACCTCAATTTCTCTGCACCTGCTGGAAGACAGTGTGATAAGAAGCAAGAGCAGCT	540				
QY	541	GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTTAAAATTAATTCCTCAAGCATTTT	600				
DB	541	GGAAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTTAAAATTAATTCCTCAAGCATTTT	600				
QY	601	GTGGAATATGATGGAACAACTCAATTTTTCGTGTACAGTTTACAGAGGTGGATAATAAT	660				
DB	601	GTGGAATATGATGGAACAACTCAATTTTTCGTGTACAGTTTACAGAGGTGGATAATAAT	660				
QY	661	GTACAGGAGCAATTTGGATAAAGTATTAAGAGGAGGATTTGGGACATATTAATCCTCCAC	720				
DB	661	GTACAGGAGCAATTTGGATAAAGTATTAAGAGGAGGATTTGGGACATATTAATCCTCCAC	720				
QY	721	TACCTGGGCTGGACCAATTTGGCCAATTTTCAGGGCCCAACAGCCCTGATTGGGCAG	780				
DB	721	TACCTGGGCTGGACCAATTTGGGCCAATTTTCAGGGCCCAACAGCCCTGATTGGGCAG	780				
QY	781	AAGCTGAGCGAGATGGACAGCGTCTCATGAAGATCCACACCTCACTGCAGTCGAAGGAG	840				
DB	781	AAGCTGAGCGAGATGGACAGCGTCTCATGAAGATCCACACCTCACTGCAGTCGAAGGAG	840				
QY	841	AGAGAGAGCGCTTTACCCAAATTTGCTGGTTCCTTTGTGGTGACCATGGCATCTCTGAACA	900				

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Db      841  AGAGAGCGCTTACCCAAATTTGCTGTTCTTTTGGTGCATGCGCATGCTGAACA 900
QY      901  GGAAGTCAAGGGGCTCTCCACCGAGGAGTGAATACACCTCTGATTTTAAATCAAGTTCT 960
Db      901  GGAAGTCAAGGGGCTCTCCACCGAGGAGTGAATACACCTCTGATTTTAAATCAAGTTCT 960
QY      961  GCGTTTGAAGGAAACCCGGTGATATCCGATATCCGATATCCGATATCCGATATCCGATAT 1020
Db      961  GCGTTTGAAGGAAACCCGGTGATATCCGATATCCGATATCCGATATCCGATATCCGATAT 1020
QY     1021  GCTGGACACTGGCGATAGACATTTGGCTTACCGATTTCCAAAGACAGTGTAGGAGCGCTC 1080
Db     1021  GCTGGACACTGGCGATAGACATTTGGCTTACCGATTTCCAAAGACAGTGTAGGAGCGCTC 1080
QY     1081  CTATTTCCAGTTTGTGAAGAGAACCAATGAGAGAGAGTTGAGATTTTACATTTGAAT 1140
Db     1081  CTATTTCCAGTTTGTGAAGAGAACCAATGAGAGAGAGTTGAGATTTTACATTTGAAT 1140
QY     1141  ACAGTGCAGCTTAGTAACTGTGCAAGAGATGTGCGCTCATATGAAAGAGATCTCTGGG 1200
Db     1141  ACAGTGCAGCTTAGTAACTGTGCAAGAGATGTGCGCTCATATGAAAGAGATCTCTGGG 1200
QY     1201  TTTGAGCAGTTTAAATGTGCAAGAGATGTGCGCTCATATGAAAGAGATCTCTGGG 1260
Db     1201  TTTGAGCAGTTTAAATGTGCAAGAGATGTGCGCTCATATGAAAGAGATCTCTGGG 1260
QY     1261  GAAAAGCATTGAGAGTCTTATTTCAACTGGGCTCCAGGTTCTCAGGAGTACCTGGAT 1320
Db     1261  GAAAAGCATTGAGAGTCTTATTTCAACTGGGCTCCAGGTTCTCAGGAGTACCTGGAT 1320
QY     1321  GCTCTGAAGACCTGAGCTTGTCCCTGAGTGCACAGTGGCGGCTTCTACCGTCTCC 1380
Db     1321  GCTCTGAAGACCTGAGCTTGTCCCTGAGTGCACAGTGGCGGCTTCTACCGTCTCC 1380
QY     1381  TGCTCAGGCTCCACAGGACCTGCACAGAAAGCTGAGTGAAGTCCACCTGTCTATCTC 1440
Db     1381  TGCTCAGGCTCCACAGGACCTGCACAGAAAGCTGAGTGAAGTCCACCTGTCTATCTC 1440
QY     1441  CTGGGTTTCTCTGCTCTTTTATTTGGTATCCTGTTCTTTTGGCGGTTACGTCATTG 1500
Db     1441  CTGGGTTTCTCTGCTCTTTTATTTGGTATCCTGTTCTTTTGGCGGTTACGTCATTG 1500
QY     1501  TGTGACCTCAGCTGAAAGTCTGCTACTTCTGCTGCTCTGCTGCTGCTGCTGCTGCTG 1560
Db     1501  TGTGACCTCAGCTGAAAGTCTGCTACTTCTGCTGCTCTGCTGCTGCTGCTGCTGCTG 1560
QY     1561  GCCTTTGCTTTACCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Db     1561  GCCTTTGCTTTTACCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
QY     1621  TGGACAGGGGCTCAGGAGAGGAGTGGAGAGCTTATCCAGGCTCTGGGTGCTGCC 1680
Db     1621  TGGACAGGGGCTCAGGAGAGGAGTGGAGAGCTTATCCAGGCTCTGGGTGCTGCC 1680
QY     1681  GACACAGTGTTCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db     1681  GACACAGTGTTCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
QY     1741  TCCTGGAGTCTTACCAAGTGTATTTAAAGAGCTGGCGGTACAGAGAGAACAGGCCCTC 1800
Db     1741  TCCTGGAGTCTTACCAAGTGTATTTAAAGAGCTGGCGGTACAGAGAGAACAGGCCCTC 1800
QY     1801  CAGCTGAGGGGCTGTGAATCGACAGCTTCCAGAGAGAGTGTGGAGTGTGAGTGTGA 1860
Db     1801  CAGCTGAGGGGCTGTGAATCGACAGCTTCCAGAGAGAGTGTGGAGTGTGAGTGTGA 1860
QY     1861  GGGAGAGAGACAAATCGGCTGACACTCAGGAGGCTCAAAAGAGAGTGTGCTGCAAC 1920
Db     1861  GGGAGAGAGACAAATCGGCTGACACTCAGGAGGCTCAAAAGAGAGTGTGCTGCAAC 1920
QY     1921  ACTCATCTGCAACCCCGAGAGTGCATCTCCCTCATCAGGTCCAGATTTCTTTTCCAAGG 1980

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Db      1921  ACTCATCTCTGCCACCCCGAGAAATGATGCTGCTCATCAGGTCCAGATTTCTTTCCAAGG 1980
QY      1981  CGGACGCTTTTCTGTTGAAATTTCTTAGTCTCTTGGCCCTCGGACACTTCACTTCGTAGTGG 2040
Db      1981  CGGACGCTTTTCTGTTGAAATTTCTTAGTCTCTTGGCCCTCGGACACTTCACTTCGTAGTGG 2040
QY     2041  GGAGTGGTGGTGAAGGAGTGAAGAGAGGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Db     2041  GGAGTGGTGGTGAAGGAGTGAAGAGAGGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
QY     2101  GGATCAAGGAGCCCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 2160
Db     2101  GGATCAAGGAGCCCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 2160
QY     2161  AGCCCTCATCTCTCTTGTGCTTGGCTTGGAGCCGTCAGAGCCCTGCTGCTGCTGCTGCTGCTGCTG 2220
Db     2161  AGCCCTCATCTCTCTTGTGCTTGGCTTGGAGCCGTCAGAGCCCTGCTGCTGCTGCTGCTGCTGCTG 2220
QY     2221  CACTCAGAGTGTGCTCATCAGGCGCACAGGCTTCTCGAGCCAGGATGATCTGTGCGCAGC 2280
Db     2221  CACTCAGAGTGTGCTCATCAGGCGCACAGGCTTCTCGAGCCAGGATGATCTGTGCGCAGC 2280
QY     2281  CTTGACCTCGGCGCCATCTGCGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
Db     2281  CTTGACCTCGGCGCCATCTGCGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
QY     2341  CTGCAACAGTATGATGTTTACCAAAAGATAAAGCGCAATTAATTCAGAAAAA 2395
Db     2341  CTGCAACAGTATGATGTTTACCAAAAGATAAAGCGCAATTAATTCAGAAAAA 2395

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RESULT 5

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US-10-063-745-139
; Sequence 139, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 139
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-745-139

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Query Match      100.0%; Score 2395; DB 13; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CCTGGAGCCGGAAGCGGGCTGACAGAGGCGGCTCCAGGTGGGGTGGGTTCGGCATC 60
Db      1  CCTGGAGCCGGAAGCGGGCTGACAGAGGCGGCTCCAGGTGGGGTGGGTTCGGCATC 60

QY     61  CAGCTAGCGTGTCCAGTACGCGCTGGGCTCGGAGCTTTTCGCTAOCCTGTTGCGTAGCG 120
Db     61  CAGCTAGCGTGTCCAGTACGCGCTGGGCTCGGAGCTTTTCGCTAOCCTGTTGCGTAGCG 120

QY    121  ATCAGAGTGTAGGATCGCGGCTTCTTCCGCGGATCTTCCCGGCTCCGCTTCGTTCC 180
Db    121  ATCAGAGTGTAGGATCGCGGCTTCTTCCGCGGATCTTCCCGGCTCCGCTTCGTTCC 180

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QY	1261	GAAAGCATTT	CAGAAGTCCT	TAATCAACCT	GGGCTCC	AAGGTTCT	CAGG	CAGTAC	CTGGAT	1320																	
DB	1261									1320																	
QY	1321	GCTCTG	AAGACG	CTGAGC	TTGTCC	CTGAGTG	CAAG	ATGGCC	CAGTTCT	CA	CCCTGCTCC	1380															
DB	1321										1380																
QY	1381	TGCTC	AGGTC	CCCA	CAGGCA	CTGC	ACAGAA	AGGCTG	AGCTG	GAAGTCC	CCACTGT	CA	CTCTC	1440													
DB	1381												1440														
QY	1441	CTGGG	TTTTCT	CGCTCT	TTTAT	TGTG	TGATCT	CTGGTTCT	TTTC	CGCG	CGTTAC	GTCA	TTG	1500													
DB	1441												1500														
QY	1501	TGTGC	ACCTC	AGCTG	AAAGTT	CTGTG	TGCTAC	TTCTGT	TGTC	CTCT	CGTGG	CTGG	CGCAG	CT	1560												
DB	1501													1560													
QY	1561	GCTTT	TGTTT	AC	GACTCT	GTGTG	AACAC	CTTG	TGTC	CAAGT	GTCT	GGCA	GTGCC	1620													
DB	1561													1620													
QY	1621	TGGAC	AGGGG	CCTC	CAGG	AAAG	AGCAG	CTGG	AGCAG	CTTAT	CC	AGGCG	CTCT	GGGT	TC	1680											
DB	1621														1680												
QY	1681	GA	CACAG	GTG	TTTCA	CA	TCTGT	CTGT	CAG	GTTCAG	ATGC	CTC	CAG	TTCT	TG	AAAG	CT	AG	TT	1740							
DB	1681																		1740								
QY	1741	TC	CTGG	CA	CTG	TATTA	CC	AA	GGTGA	TTTAA	AAG	CTTGG	CGGT	CA	CAG	AG	AA	CAAG	CCCC	1800							
DB	1741																		1800								
QY	1801	CAG	CTCAG	GGG	GTGTG	TGA	ATCCG	AGCAG	CTCC	CC	AGCAG	AGG	GTGG	AG	CTG	CAG	CTGA	1860									
DB	1801																	1860									
QY	1861	GGG	AAAG	AG	AGCA	AA	TCGG	CTTG	GA	CA	TC	AGG	AGG	TC	CA	AA	AG	AG	ACT	TG	TC	GC	AC	1920			
DB	1861																						1920				
QY	1921	ACT	CAT	CTCG	CA	CCCC	CC	AG	ATGC	ATCT	GC	CTCAT	CAG	GTCC	AG	ATTTCT	TT	CC	CA	AG	1980						
DB	1921																			1980							
QY	1981	CGG	ACG	TTTTCT	CT	TG	GA	ATTTCT	TAG	TC	CT	CG	CTCG	AG	CA	CTTCA	TT	CG	T	AG	CT	GG	2040				
DB	1981																			2040							
QY	2041	GG	AG	TG	TG	TG	AGG	CA	GTGA	AG	AG	CG	GA	TG	TC	AC	AT	CAG	AT	CC	AG	AG	CC	CA	2100		
DB	2041																			2100							
QY	2101	GG	ATCA	AGG	CA	CCCC	ACTG	CA	GTG	CG	CA	AG	CA	GA	CTGT	TG	GG	CCCC	CC	CA	CCCC	CA	CC	CT	GC	AC	2160
DB	2101																			2160							
QY	2161	AG	CC	CTCAT	CCCC	CT</																					

181	QY	TCTGCCAGCGGAAACACGGAGCGGAGCCGCCAGCGCCCGAAACCCCTCGGTGGAGCGCACT	240
181	Db		
181	QY	TCTGCCAGCGGAAACACGGAGCGGAGCCGCCAGCGCCCGAAACCCCTCGGTGGAGCGCACT	240
181	Db		
241	QY	TCTAACTCGACACGCTGCCACACCTCTCTTCAGTAAAGTGTGTATTTGTTCTGTATAGAT	300
241	Db		
241	QY	TCTAACTCGACACGCTGCCACACCTCTCTTCAGTAAAGTGTGTATTTGTTCTGTATAGAT	300
241	Db		
301	QY	GCCTTGGAGAGATGATTTTGTGTTTGGGTCAAGGGTGTGAAATTTATGCCCTACACAAC	360
301	Db		
301	QY	GCCTTGGAGAGATGATTTTGTGTTTGGGTCAAGGGTGTGAAATTTATGCCCTACACAAC	360
301	Db		
361	QY	TACCTTGTGGAAGAGGAGCATCTCACAGTTTGTGCTGAGCAAGACCAACCTACAGTT	420
361	Db		
361	QY	TACCTTGTGGAAGAGGAGCATCTCACAGTTTGTGCTGAGCAAGACCAACCTACAGTT	420
361	Db		
421	QY	ACTATGCCCTCGAATCAAGCATTTGATGACGGGAGCCTTCTCGCTTTGTGCGAGTCATC	480
421	Db		
421	QY	ACTATGCCCTCGAATCAAGCATTTGATGACGGGAGCCTTCTCGCTTTGTGCGAGTCATC	480
421	Db		
481	QY	AGGAACCTCAATTTCTCTCTGCACTGCTGGAAGACAGTGTGATTAAGACAAAGACAGCT	540
481	Db		
481	QY	AGGAACCTCAATTTCTCTCTGCACTGCTGGAAGACAGTGTGATTAAGACAAAGACAGCT	540
481	Db		
541	QY	GGAAAGAAGATAGTCTTTTATCGGATGAAACCTCGGTTAAATTTATCCCAAAGCATTTT	600
541	Db		
541	QY	GGAAAGAAGATAGTCTTTTATCGGATGAAACCTCGGTTAAATTTATCCCAAAGCATTTT	600
541	Db		
601	QY	GTGGAATATGATGGAAACACCTCATTTTTCGTGTCAGATTACAGAGGTGGATAAAT	660
601	Db		
601	QY	GTGGAATATGATGGAAACACCTCATTTTTCGTGTCAGATTACAGAGGTGGATAAAT	660
601	Db		
661	QY	GTCAAGGCAATTTGGATAAAGTATTAAGAGGAGATTGGACATATTAATCTCCAC	720
661	Db		
661	QY	GTCAAGGCAATTTGGATAAAGTATTAAGAGGAGATTGGACATATTAATCTCCAC	720
661	Db		
721	QY	TACTGGGGCTGCACACATTTGCGCCCAATTTGAGGCCCAACAGGCCCTGATTTGGCGAG	780
721	Db		
721	QY	TACTGGGGCTGCACACATTTGCGCCCAATTTGAGGCCCAACAGGCCCTGATTTGGCGAG	780
721	Db		
781	QY	AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACCTCAGTCAGTCGAAGAG	840
781	Db		
781	QY	AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACCTCAGTCAGTCGAAGAG	840
781	Db		
841	QY	AGAGAGCGCTTTTACCCCAATTTGCTGTTCTTTGTGTGTGACCATGGCATGTCTGAAACA	900
841	Db		
841	QY	AGAGAGCGCTTTTACCCCAATTTGCTGTTCTTTGTGTGTGACCATGGCATGTCTGAAACA	900
841	Db		
901	QY	GGAAAGTCAACGGGGCTCTCTCCAGGAGGAGTGAATACACCTTGATTTAATCAGTTCT	960
901	Db		
901	QY	GGAAAGTCAACGGGGCTCTCTCCAGGAGGAGTGAATACACCTTGATTTAATCAGTTCT	960
901	Db		
961	QY	CGCTTTGAAAGGAAACCGGTGATATCCGACATCCAAAGCACGCTCCAAATAGACGGATGTG	1020
961	Db		
961	QY	CGCTTTGAAAGGAAACCGGTGATATCCGACATCCAAAGCACGCTCCAAATAGACGGATGTG	1020
961	Db		
1021	QY	GCTCGCACCTGGCGATAGCATTTGGCTTACCAGATTCCAAAGACAGTGTAGGGAGCCTC	1080
1021	Db		
1021	QY	GCTCGCACCTGGCGATAGCATTTGGCTTACCAGATTCCAAAGACAGTGTAGGGAGCCTC	1080
1021	Db		
1081	QY	CTATTCCAGTTGTGGAGGAGGAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
1081	Db		
1081	QY	CTATTCCAGTTGTGGAGGAGGAGACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
1081	Db		
1141	QY	ACAGTGCAGCTTAGTAAACTGTTCCAAAGAGATGTGCCGTATATGAAAAGATCTCTGGG	1200
1141	Db		
1141	QY	ACAGTGCAGCTTAGTAAACTGTTCCAAAGAGATGTGCCGTATATGAAAAGATCTCTGGG	1200
1141	Db		
1201	QY	TTTGGAGCGTTTAAATGTCAAGAGATTCATCGGAGACTGGATCAGCTGTACTTTGGAG	1260
1201	Db		
1201	QY	TTTGGAGCGTTTAAATGTCAAGAGATTCATCGGAGACTGGATCAGCTGTACTTTGGAG	1260
1201	Db		

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|||||
Db 2341 CTGCACACGATGATAGTATCCAAAGAAATTAACGGCAATTAATGAGAAAAA 2395
|||||

RESULT 6
US-10-063-513-139
; Sequence 139, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 139
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-139

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Query Match 100.0%; Score 2395; DB 13; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCGAGCGGAAGCGGGCTGACGAGCGGAGGCTCCAGGTGGGTCGGTTCGGCATC 60
Db 1 CCTGGAGCGGAAGCGGGCTGACGAGCGGAGGCTCCAGGTGGGTCGGTTCGGCATC 60
QY 61 CAGCCTAGCGTGTCCAGATCGGCTGGGCTCCGGGACTTTCGCTACCTGTTCGGTAGCG 120
Db 61 CAGCCTAGCGTGTCCAGATCGGCTGGGCTCCGGGACTTTCGCTACCTGTTCGGTAGCG 120
QY 121 ATCGAGTGTAGGATCGGGTCTTCTTCGGGATCTTCCGGGCTCCGGTTCGGTTC 180
Db 121 ATCGAGTGTAGGATCGGGTCTTCTTCGGGATCTTCCGGGCTCCGGTTCGGTTC 180
QY 181 TCTGCCAGAGCGGAACACGAGCGGAGCGCCCGGAGCGGCTCCGGTTCGGTTC 240
Db 181 TCTGCCAGAGCGGAACACGAGCGGAGCGCCCGGAGCGGCTCCGGTTCGGTTC 240
QY 241 TCTAACTGGACCGCTGCCACACCTCTCTTCAGTAAAGTTGTTATTTCTGATAGAT 300
Db 241 TCTAACTGGACCGCTGCCACACCTCTCTTCAGTAAAGTTGTTATTTCTGATAGAT 300
QY 301 GCCTTGAGAGATGATTTTGTGTTGGTTCAGAGGTTGAAATTAATGCCCCACAACT 360
Db 301 GCCTTGAGAGATGATTTTGTGTTGGTTCAGAGGTTGAAATTAATGCCCCACAACT 360
QY 361 TACCTTGGAAGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCAAGCACTACAGTT 420
Db 361 TACCTTGGAAGAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCAAGCACTACAGTT 420
QY 421 ACTATGCCATCAAGGCAATGATGACGGGAGCGCTTCTGCTTTGTCGAGTCATC 480
Db 421 ACTATGCCATCAAGGCAATGATGACGGGAGCGCTTCTGCTTTGTCGAGTCATC 480
QY 481 AGGAACCTCAATCTCTGCACTGCTGGAAGACAGTGTGATGAACCAAGCAAGCACT 540
Db 481 AGGAACCTCAATCTCTGCACTGCTGGAAGACAGTGTGATGAACCAAGCAAGCACT 540
QY 541 GGAAAAAGAAATAGTCTTTTATGAGATGAAACCTCGGGTTAAATTAATCCCAAGCATTTT 600
Db 541 GGAAAAAGAAATAGTCTTTTATGAGATGAAACCTCGGGTTAAATTAATCCCAAGCATTTT 600

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Db 541 GGAAAAAGAAATAGTCTTTTATGAGATGAAACCTCGGGTTAAATTAATCCCAAGCATTTT 600
QY 601 GTGGAATATGATGGAACAAACCTCATTTTTCGTGTGATGATTAACAGAGGTGATTAAT 660
Db 601 GTGGAATATGATGGAACAAACCTCATTTTTCGTGTGATGATTAACAGAGGTGATTAAT 660
QY 661 GTCCAGAGGCATTTGGATATAAGTATTAATAAGAGAGATGGGACATTAATCTCCAC 720
Db 661 GTCCAGAGGCATTTGGATATAAGTATTAATAAGAGAGATGGGACATTAATCTCCAC 720
QY 721 TACCTGGGCTGGACCAATTTGGCCACATTTTCAGGGCCCAACAGCCCTCATTTGGGAG 780
Db 721 TACCTGGGCTGGACCAATTTGGCCACATTTTCAGGGCCCAACAGCCCTCATTTGGGAG 780
QY 781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGACGTCCGAAGAG 840
Db 781 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGACGTCCGAAGAG 840
QY 841 AGAGAGCGCTTTACCCAAATTTCTGTTCTTTTGTGTGACCATGGCATCTCTGAACA 900
Db 841 AGAGAGCGCTTTACCCAAATTTCTGTTCTTTTGTGTGACCATGGCATCTCTGAACA 900
QY 901 GGAAGTCAAGGGGCTCTCCACCGAGAGGTGAATACACCTCTGATTTTAAATCAGTTCT 960
Db 901 GGAAGTCAAGGGGCTCTCTCCACCGAGAGGTGAATACACCTCTGATTTTAAATCAGTTCT 960
QY 961 GCGTTTGAAGGAAACCGGTGATATCCGACATCCAAAGACGTCCTCAATAGACGGATGTG 1020
Db 961 GCGTTTGAAGGAAACCGGTGATATCCGACATCCAAAGACGTCCTCAATAGACGGATGTG 1020
QY 1021 GCTCGGACATGCGGATAGACTTTGGCTTACCGATTCGAAAGACAGTGTAGGAGCCTC 1080
Db 1021 GCTCGGACATGCGGATAGACTTTGGCTTACCGATTCGAAAGACAGTGTAGGAGCCTC 1080
QY 1081 CTATTTCCAGTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Db 1081 CTATTTCCAGTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 ACAGTGCAGCTTAGTAAACTGTTTCAAGAGATGTCGCTCATATGAAAGAGATCCTGGG 1200
Db 1141 ACAGTGCAGCTTAGTAAACTGTTTCAAGAGATGTCGCTCATATGAAAGAGATCCTGGG 1200
QY 1201 TTTGAGCAGTTTAAATATGTCGAAAGATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
Db 1201 TTTGAGCAGTTTAAATATGTCGAAAGATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
QY 1261 GAAAGCATTCAGAGGCTTATTCACCTGGGCTCCAGGTTCTCAGGCGAGTACCTGGAT 1320
Db 1261 GAAAGCATTCAGAGGCTTATTCACCTGGGCTCCAGGTTCTCAGGCGAGTACCTGGAT 1320
QY 1321 GCTCTGAAGAGCTGAGCTTGTCTGAGTGCACAAGTGGGCGCCAGTTCTCACCCCTGCTCC 1380
Db 1321 GCTCTGAAGAGCTGAGCTTGTCTGAGTGCACAAGTGGGCGCCAGTTCTCACCCCTGCTCC 1380
QY 1381 TGCTCAGGCTCCACAGGCACTGCAGAGAGGCTGAGCTGGAAGTCCCACTGTCATCTC 1440
Db 1381 TGCTCAGGCTCCACAGGCACTGCAGAGAGGCTGAGCTGGAAGTCCCACTGTCATCTC 1440
QY 1441 CTGGGTTTCTCTGCTCTTTTATTTGTTGATCTTGGTTCTTTTCGGCGCTTCCAGCTCATG 1500
Db 1441 CTGGGTTTCTCTGCTCTTTTATTTGTTGATCTTGGTTCTTTTCGGCGCTTCCAGCTCATG 1500
QY 1501 TGTGCACTCAGCTGAAAGTTGCTGCTTCTTGTGCTTCTGCTGCTTCTGCTGCTGCTGCTG 1560
Db 1501 TGTGCACTCAGCTGAAAGTTGCTGCTTCTTGTGCTTCTGCTGCTTCTGCTGCTGCTGCTG 1560
QY 1561 GCCTTTGTTTACAGACTCTGTTGAAACACCTGTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Db 1561 GCCTTTGTTTACAGACTCTGTTGAAACACCTGTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
QY 1621 TGGACAGGGGCTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
Db 1621 TGGACAGGGGCTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680

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QY 1681 GACACAGGTGTTCACTCTGTGTGTGTCAGGTGTCAGATGCTCAGTCTTCTGGAAGCTAGGT 1740
DB 1681 GACACAGGTGTTCACTCTGTGTGTGTCAGGTGTCAGATGCTCAGTCTTCTGGAAGCTAGGT 1740
QY 1741 TCCTGGACCTGTTACCAAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAAGCCGCC 1800
DB 1741 TCCTGGACCTGTTACCAAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAAGCCGCC 1800
QY 1801 CAGCTGAGGGGGTGTGTAATCGGACAGCTCCAGCAGAGAGGTGTGGAGCTGCAAGTGA 1860
DB 1801 CAGCTGAGGGGGTGTGTAATCGGACAGCTCCAGCAGAGAGGTGTGGAGCTGCAAGTGA 1860
QY 1861 GGGGAAGAAGACAAATCGGCTGGACACTCAGAGGGTCAAAAGAGACTTGTGCGAC 1920
DB 1861 GGGGAAGAAGACAAATCGGCTGGACACTCAGAGGGTCAAAAGAGACTTGTGCGAC 1920
QY 1921 ACTCATCTGCGACCCAGCAATGATCTCTGCTCATCAGGTCCAGATTTCTTCCAAAG 1980
DB 1921 ACTCATCTGCGACCCAGCAATGATCTCTGCTCATCAGGTCCAGATTTCTTCCAAAG 1980
QY 1981 CGGACGTTTTCTGTTGGAATCTTAGTCTTGGCTCGGACACCTTCAATTCGTTAGCTGG 2040
DB 1981 CGGACGTTTTCTGTTGGAATCTTAGTCTTGGCTCGGACACCTTCAATTCGTTAGCTGG 2040
QY 2041 GGAGTGGTGGAGCAGTGAAGAAGAGCGGATGTCACCTCAGATCCACAGAGCCCA 2100
DB 2041 GGAGTGGTGGAGCAGTGAAGAAGAGCGGATGTCACCTCAGATCCACAGAGCCCA 2100
QY 2101 GGATCAAGGACCCACTGCGAGTGGCAGAGGACTGTTGGGCCCCCACCACCCCTGCGAC 2160
DB 2101 GGATCAAGGACCCACTGCGAGTGGCAGAGGACTGTTGGGCCCCCACCACCCCTGCGAC 2160
QY 2161 AGCCCTCATCCCTCTTGGCTTTAGCCGTCAGAGGCCCTGTGCTCAGTGTCTGACCGAGA 2220
DB 2161 AGCCCTCATCCCTCTTGGCTTTAGCCGTCAGAGGCCCTGTGCTCAGTGTCTGACCGAGA 2220
QY 2221 CACTCAGAGTGTGTCATCAGGGCAGAGCTTCTCGGAGCAGGATGATCTGCGCAG 2280
DB 2221 CACTCAGAGTGTGTCATCAGGGCAGAGCTTCTCGGAGCAGGATGATCTGCGCAG 2280
QY 2281 CTTGACCTCGGGCCCATCTGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG 2340
DB 2281 CTTGACCTCGGGCCCATCTGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG 2340
QY 2341 CTGCAACAGTATGTAGTTACCAAAAGATAAAGCGCAATTAATGAGAAAAAAA 2395
DB 2341 CTGCAACAGTATGTAGTTACCAAAAGATAAAGCGCAATTAATGAGAAAAAAA 2395

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RESULT 7

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US-10-063-569-139
; Sequence 139, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; PENDING FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 139
; LENGTH: 2395

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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-569-139

Query Match      100.0%; Score 2395; DB 13; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGAGCCGGAAGCGGGCTGACGAGCGGCGAGGCTCAGGTGGGGTGGGTTCGGATC 60
DB 1 CCTGGAGCCGGAAGCGGGCTGACGAGCGGCGAGGCTCAGGTGGGGTGGGTTCGGATC 60
QY 61 CAGCTAGCTGTGTCCACGATCGGCTGGGCTCCCGGACTTTTCGTACCTGTTCGTAGCG 120
DB 61 CAGCTAGCTGTGTCCACGATCGGCTGGGCTCCCGGACTTTTCGTACCTGTTCGTAGCG 120
QY 121 ATCGAGGTGTAGGGATCGCGGTCTTCTTCCGGGGATTTCTTCCGGCTCCCGTTCGTTCC 180
DB 121 ATCGAGGTGTAGGGATCGCGGTCTTCTTCCGGGGATTTCTTCCGGCTCCCGTTCGTTCC 180
QY 181 TCTGCCAGCGGAACACGAGCGGAGCCGCCAGCGCCCGAACCCTCGCTGAGCCAGT 240
DB 181 TCTGCCAGCGGAACACGAGCGGAGCCGCCAGCGCCCGAACCCTCGCTGAGCCAGT 240
QY 241 TCTAACTGGACACGCTGCCACCACTCTCTTCAAGTAAAGTTGTTTATTTCTGTAGAT 300
DB 241 TCTAACTGGACACGCTGCCACCACTCTCTTCAAGTAAAGTTGTTTATTTCTGTAGAT 300
QY 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAGGGTGTGAATTTATGCCCTACACAACT 360
DB 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAGGGTGTGAATTTATGCCCTACACAACT 360
QY 361 TACCTTGTGAAAAAGGAGAGCATCTCACAGTTTGTGGCTGGAAGCAAGCAAGCAAGCACT 420
DB 361 TACCTTGTGAAAAAGGAGAGCATCTCACAGTTTGTGGCTGGAAGCAAGCAAGCAAGCACT 420
QY 421 ACTATGCTCGAATCAAGGCAATTGATGACGGGAGCTTCTTCTGGCTTGTTCGACGTATC 480
DB 421 ACTATGCTCGAATCAAGGCAATTGATGACGGGAGCTTCTTCTGGCTTGTTCGACGTATC 480
QY 481 AGGAACCTCAATTTCTTCGCTGCTGGAAGAGAGTGTGATGAAGCAAGCAAGCAAGCACT 540
DB 481 AGGAACCTCAATTTCTTCGCTGCTGGAAGAGAGTGTGATGAAGCAAGCAAGCAAGCACT 540
QY 541 GGAAGAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTTAAATTAATTCGCAAGCAATTT 600
DB 541 GGAAGAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTTAAATTAATTCGCAAGCAATTT 600
QY 601 GTGGAATATGATGGAACAAACCTTCTTTCGTGTGAGATTAACAGAGGTGGGATAAAT 660
DB 601 GTGGAATATGATGGAACAAACCTTCTTTCGTGTGAGATTAACAGAGGTGGGATAAAT 660
QY 661 GTGGAATATGATGGAACAAACCTTCTTTCGTGTGAGATTAACAGAGGTGGGATAAAT 720
DB 661 GTGGAATATGATGGAACAAACCTTCTTTCGTGTGAGATTAACAGAGGTGGGATAAAT 720
QY 721 TACCTGGGCTGGACCAACATTTGGCCCACTTTTCAAGGCCCAAGCAAGCCCTGATGGGCGAG 780
DB 721 TACCTGGGCTGGACCAACATTTGGCCCACTTTTCAAGGCCCAAGCAAGCCCTGATGGGCGAG 780
QY 781 AAGCTGAGGAGATGACAGAGCGTGTGATGAAGATCCACCTCTCTGAGTGTGAGAGGAG 840
DB 781 AAGCTGAGGAGATGACAGAGCGTGTGATGAAGATCCACCTCTCTGAGTGTGAGAGGAG 840
QY 841 AGAGAGACCTTTTACCCAAATTTGCTGTTCTTTTGTGGTGAACCATGGCATGTCTGAAACA 900
DB 841 AGAGAGACCTTTTACCCAAATTTGCTGTTCTTTTGTGGTGAACCATGGCATGTCTGAAACA 900
QY 901 GGAAGTACAGGGGCTCTTCCACCGAGAGGTGAATACACCTCTGATTTTAAATCAGTTCT 960
DB 901 GGAAGTACAGGGGCTCTTCCACCGAGAGGTGAATACACCTCTGATTTTAAATCAGTTCT 960
QY 961 GCGTTTGAAGAGGAACCCCGGTGATATCCGACATCCCAAGCAGCTCCCAATAGACGAGTGTG 1020

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[illegible]

RESULT 8

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US-10-063-551-139
; Sequence 139, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1c1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 139
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-139

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Query Match	100.0%;	Score 2395;	DB 13;	Length 2395;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2395;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CTTGGAGCCGGAACGCGGCTGCAGCAGGCGCAGGCTCCAGGTGGGGTCGGTTCGGATC	60	
Db	1	CTTGGAGCCGGAACGCGGCTGCAGCAGGCGCAGGCTCCAGGTGGGGTCGGTTCGGATC	60	
QY	61	CAGCCTTAGCGTGTCCAGGATCGCGCTGGGCTCCGGGACTTTTCGTA	120	
Db	61	CAGCCTTAGCGTGTCCAGGATCGCGCTGGGCTCCGGGACTTTTCGTA	120	
QY	121	ATCGAGGTGCTAGGGATCGCGGTCTTCTTCGGGGGATCTTTC	180	
Db	121	ATCGAGGTGCTAGGGATCGCGGTCTTCTTCGGGGGATCTTTC	180	
QY	181	CTTGCACAGACCGGAACACGAGCGGAGCCCGCAGCGCCCGAA	240	
Db	181	CTTGCACAGACCGGAACACGAGCGGAGCCCGCAGCGCCCGAA	240	
QY	241	TCTAACTGGACACCGGTGCCACCACTCTCTTCAGTAAAGTTGTAT	300	
Db	241	TCTAACTGGACACCGGTGCCACCACTCTCTTCAGTAAAGTTGTAT	300	

QY 301 GCCTTGAGAGATGATTTTGTGTTTGGCTCAAGGGTGTGAATTTATGCCCTACACAAC 360
 Db 301 GCCTTGAGAGATGATTTTGTGTTTGGCTCAAGGGTGTGAATTTATGCCCTACACAAC 360
 QY 361 TACCTTGCGAAAAGAGAGATCTCACAGTTTGTGGCTGAAGCAAGCAACCACTACAGTT 420
 Db 361 TACCTTGCGAAAAGAGAGATCTCACAGTTTGTGGCTGAAGCAAGCAACCACTACAGTT 420
 QY 421 ACTATGCTCGAATCAAGGCATTAAGACGGGAGCCCTTCTGCTTGTGAGCTCATC 480
 Db 421 ACTATGCTCGAATCAAGGCATTAAGACGGGAGCCCTTCTGCTTGTGAGCTCATC 480
 QY 481 AGGAACCTCAATCTCTGCACTGCTGAAGACAGTGTGAAGACAGCAAGCAAGCAAGCT 540
 Db 481 AGGAACCTCAATCTCTGCACTGCTGAAGACAGTGTGAAGACAGCAAGCAAGCAAGCT 540
 QY 541 GGAAGAAAGATAGTCTTTTATGGAGATGAACCTGGGTAAATTTATCCCAAGCATTTT 600
 Db 541 GGAAGAAAGATAGTCTTTTATGGAGATGAACCTGGGTAAATTTATCCCAAGCATTTT 600
 QY 601 GTGAATATGATGAAGCAACCTCTATTTTCTGTCAGATTACACAGAGGTGGATAAAT 660
 Db 601 GTGAATATGATGAAGCAACCTCTATTTTCTGTCAGATTACACAGAGGTGGATAAAT 660
 QY 661 GTGAGGAGATGAGCAAGCTGCTGATGAAGATCCACCTCTACTGAGTGGAGGAG 840
 Db 661 GTGAGGAGATGAGCAAGCTGCTGATGAAGATCCACCTCTACTGAGTGGAGGAG 840
 QY 721 TACCTGGGGCTGGACCAATTTGGCCACATTTTCAAGGGCCCAACAGCCCTGATTTGGG 780
 Db 721 TACCTGGGGCTGGACCAATTTGGCCACATTTTCAAGGGCCCAACAGCCCTGATTTGGG 780
 QY 781 AAGTGAGCGAGATGAGCAAGCTGCTGATGAAGATCCACCTCTACTGAGTGGAGGAG 840
 Db 781 AAGTGAGCGAGATGAGCAAGCTGCTGATGAAGATCCACCTCTACTGAGTGGAGGAG 840
 QY 841 AGAGAGCGCTTTACCAATTTGCTGTTCTTGTGAGCATGTCGAAACA 900
 Db 841 AGAGAGCGCTTTACCAATTTGCTGTTCTTGTGAGCATGTCGAAACA 900
 QY 901 GGAAGTACGGGGCTCTCTCCACCGAGAGTGAATACACCTCTGATTTTAAATGATTTCT 960
 Db 901 GGAAGTACGGGGCTCTCTCCACCGAGAGTGAATACACCTCTGATTTTAAATGATTTCT 960
 QY 961 GGGTTTGAAGAGAAACCCGGTGATATCCGACATCCAAAGCAGTCCAAATAGACGGATGT 1020
 Db 961 GGGTTTGAAGAGAAACCCGGTGATATCCGACATCCAAAGCAGTCCAAATAGACGGATGT 1020
 QY 1021 GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 1080
 Db 1021 GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTC 1080
 QY 1081 CTATTTCCAGTTTGGAGGAAGACCAATGAGAGAGAGTTCAGATTTTATCATTTGAT 1140
 Db 1081 CTATTTCCAGTTTGGAGGAAGACCAATGAGAGAGAGTTCAGATTTTATCATTTGAT 1140
 QY 1141 ACAGTGACGCTTGTAAATCTGTCAGAGAGATGTCGCTCATATGAAGAGATCTGGG 1200
 Db 1141 ACAGTGACGCTTGTAAATCTGTCAGAGAGATGTCGCTCATATGAAGAGATCTGGG 1200
 QY 1201 TTTGAGCAGTTTAAATGTGAGAGAGATGTCGCTCATATGAAGAGATCTGGG 1260
 Db 1201 TTTGAGCAGTTTAAATGTGAGAGAGATGTCGCTCATATGAAGAGATCTGGG 1260
 QY 1261 GAAAAGCATTCAGAGTCTTATTAACCTGGGTCCAGAGTTCAGGAGTACCTGGAT 1320
 Db 1261 GAAAAGCATTCAGAGTCTTATTAACCTGGGTCCAGAGTTCAGGAGTACCTGGAT 1320
 QY 1321 GCTCTGAAGACGCTGAGCTTGTCTCTGAGTGACAGTGGCCGAGTTCACCTGCTCC 1380
 Db 1321 GCTCTGAAGACGCTGAGCTTGTCTCTGAGTGACAGTGGCCGAGTTCACCTGCTCC 1380

QY 1381 TGCTACGCTGCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAAGTCCCACTGTCTATCTC 1440
 Db 1381 TGCTACGCTGCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAAGTCCCACTGTCTATCTC 1440
 QY 1441 CTGGGTTTTCTGCTCTTTTATTTTGGTGTATCCCTGGTTCTTTCCGCCGTTTCACTGCTATG 1500
 Db 1441 CTGGGTTTTCTGCTCTTTTATTTTGGTGTATCCCTGGTTCTTTCCGCCGTTTCACTGCTATG 1500
 QY 1501 TGTGCACTCAGCTGAAAGTTGCTGTCTTCTGTGGCTCTCTGCTGGCTGCGGCAAGCT 1560
 Db 1501 TGTGCACTCAGCTGAAAGTTGCTGTCTTCTGTGGCTCTCTGCTGGCTGCGGCAAGCT 1560
 QY 1561 GCCTTTCTGTTTACAGACTCTGCTGTGAACACTCTGCTGTGCAAGTCTGCTGGAGTGCCTC 1620
 Db 1561 GCCTTTCTGTTTACAGACTCTGCTGTGAACACTCTGCTGTGCAAGTCTGCTGGAGTGCCTC 1620
 QY 1621 TGGACAGGGGCTCAGGAGAGGAGCTGGAGAGGAGCTTATCCAGGCTCTGCTGGTGTCTCC 1680
 Db 1621 TGGACAGGGGCTCAGGAGAGGAGCTGGAGAGGAGCTTATCCAGGCTCTGCTGGTGTCTCC 1680
 QY 1681 GACACAGGTGTTACATCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
 Db 1681 GACACAGGTGTTACATCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
 QY 1741 TCCTGGCAGCTGTTACCAAGGTGATTTAAAGAGCTGGCGGTCAAGAGAAACAAGCCCTC 1800
 Db 1741 TCCTGGCAGCTGTTACCAAGGTGATTTAAAGAGCTGGCGGTCAAGAGAAACAAGCCCTC 1800
 QY 1801 CAGCTGAGGGGCTGTTGAATCGGACAGCTCCAGCAGAGCTGTTGGAGCTGCAAGCTGA 1860
 Db 1801 CAGCTGAGGGGCTGTTGAATCGGACAGCTCCAGCAGAGCTGTTGGAGCTGCAAGCTGA 1860
 QY 1861 GGGAGAGAGAGACAAATCGGCTTGGACACTCAGGAGGCTCAAAAGAGAGACTTGGTCCGACC 1920
 Db 1861 GGGAGAGAGAGACAAATCGGCTTGGACACTCAGGAGGCTCAAAAGAGAGACTTGGTCCGACC 1920
 QY 1921 ACTCATCTGCTGCTCCAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
 Db 1921 ACTCATCTGCTGCTCCAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
 QY 1981 CGGAGTCTTCTGTTTGGAAATCTTAGTCTTGGCTCGGACACCTTCAATCTGTTAGCTGG 2040
 Db 1981 CGGAGTCTTCTGTTTGGAAATCTTAGTCTTGGCTCGGACACCTTCAATCTGTTAGCTGG 2040
 QY 2041 GGAAGTGTGCTGAGCAGTGAAGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
 Db 2041 GGAAGTGTGCTGAGCAGTGAAGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
 QY 2101 GGAACAGGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
 Db 2101 GGAACAGGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
 QY 2161 AGCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
 Db 2161 AGCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
 QY 2221 CACTCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
 Db 2221 CACTCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
 QY 2281 CTGTCAGCTCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
 Db 2281 CTGTCAGCTCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
 QY 2341 CTGTCACAGTATGATGTTTACCAAGAGAAATAACGCAATAATTGAGAAAAAAA 2395
 Db 2341 CTGTCACAGTATGATGTTTACCAAGAGAAATAACGCAATAATTGAGAAAAAAA 2395

661	Db	GTCAAGGCAATTTGGATAAAGTATTAAAGAGGAGATTGGGACATATTAACTCCTCCAC	720
721	Qy	TACCTGGGGCTGGACCACCATTTGGCCCATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAG	780
721	Db	TACCTGGGGCTGGACCACCATTTGGCCCATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAG	780
781	Qy	AAGCTGAGCGAGATGACACAGCGTGTGATGAAGATCCACACCTCACTGCGAGTCGAAGAG	840
781	Db	AAGCTGAGCGAGATGACACAGCGTGTGATGAAGATCCACACCTCACTGCGAGTCGAAGAG	840
841	Qy	AGAGAGCGCTTTACCCAAATTTGCTGGTCTTTGTGTGTGACCAATGCATCTCTGGAACA	900
841	Db	AGAGAGCGCTTTACCCAAATTTGCTGGTCTTTGTGTGTGACCAATGCATCTCTGGAACA	900
901	Qy	GGAAAGTCACGGGGCCTCCTCCACGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCT	960
901	Db	GGAAAGTCACGGGGCCTCCTCCACGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCT	960
961	Qy	GGCTTTGAAAGGAAAACCCGGTGATATCCGCATCTCCAAAGCAGTCCAAATAGACGGATGTG	1020
961	Db	GGCTTTGAAAGGAAAACCCGGTGATATCCGCATCTCCAAAGCAGTCCAAATAGACGGATGTG	1020
1021	Qy	GCTGCGACACTGGCGATAGCACTGGCTTACCGATTCCTAAAGACAGCTGAGGAGCGCTC	1080
1021	Db	GCTGCGACACTGGCGATAGCACTGGCTTACCGATTCCTAAAGACAGCTGAGGAGCGCTC	1080
1081	Qy	CTATTCCTCAGTTGTGGAAGGAAGACCAATCAGAGAGCAGTTGAGATTTTACATTTGAAAT	1140
1081	Db	CTATTCCTCAGTTGTGGAAGGAAGACCAATCAGAGAGCAGTTGAGATTTTACATTTGAAAT	1140
1141	Qy	ACAGTCAGCTTTAGTAAACTTTGTCAGAGAAATGTGCCGTCAATGAAAAAGATCCTGGG	1200
1141	Db	ACAGTCAGCTTTAGTAAACTTTGTCAGAGAAATGTGCCGTCAATGAAAAAGATCCTGGG	1200
1201	Qy	TTTTCAGCAGTTTAAATGTGAGAAAGATTCGATGGGAACCTGGATCAGACTGTCTGGAG	1260
1201	Db	TTTTCAGCAGTTTAAATGTGAGAAAGATTCGATGGGAACCTGGATCAGACTGTCTGGAG	1260
1261	Qy	GAAGAAGTTCAGAGTCTTATTCAACCTGGGCTCCAAAGTTCTCAGGCAAGTACCTGGAT	1320
1261	Db	GAAGAAGTTCAGAGTCTTATTCAACCTGGGCTCCAAAGTTCTCAGGCAAGTACCTGGAT	1320
1321	Qy	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCCAGTTTCTCACCTGTCTCC	1380
1321	Db	GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCCAGTTTCTCACCTGTCTCC	1380
1381	Qy	TGCTCAGCTGCCACAGGCACTGCAAGAAAGCTGAGCTGGAAGTCCCACTGTCTATCTC	1440
1381	Db	TGCTCAGCTGCCACAGGCACTGCAAGAAAGCTGAGCTGGAAGTCCCACTGTCTATCTC	1440
1441	Qy	CTGGTTTCTCTGCTCTCTTTATTGTTGATCTGTGGTTCTTTGGCGCGTTCACTGATG	1500
1441	Db	CTGGTTTCTCTGCTCTCTTTATTGTTGATCTGTGGTTCTTTGGCGCGTTCACTGATG	1500
1501	Qy	TGTGCACCTCAGCTGAAAGTTCTGTCTGCTGTGCTCTCTGTGCTGCGGCAAGCT	1560
1501	Db	TGTGCACCTCAGCTGAAAGTTCTGTCTGCTGTGCTCTCTGTGCTGCGGCAAGCT	1560
1561	Qy	GCCTTTTGTTTACGAGACTCTGTTGAAACACTGGTGTGTGCCAAGTGTCTGGCAGTGCCT	1620
1561	Db	GCCTTTTGTTTACGAGACTCTGTTGAAACACTGGTGTGTGCCAAGTGTCTGGCAGTGCCT	1620
1621	Qy	TGGACAGGGGGCCTCAGGGAAGGACGTGGAGAGCCCTTATCCCAAGGCTCTGGGTGTCCC	1680
1621	Db	TGGACAGGGGGCCTCAGGGAAGGACGTGGAGAGCCCTTATCCCAAGGCTCTGGGTGTCCC	1680
1681	Qy	GACACAGGTGTTACATCTGCTGTGTGCTCAGGTTCAGATGCCTCAGTTCTTGGAAGCTAGGT	1740
1681	Db	GACACAGGTGTTACATCTGCTGTGTGCTCAGGTTCAGATGCCTCAGTTCTTGGAAGCTAGGT	1740
1741	Qy	TCCTGCGACTGTTTACCAAGGTGATTTGAAAGCTGTCGCGTTCACAGAGGAACAAGCCCCC	1800
1741	Db	TCCTGCGACTGTTTACCAAGGTGATTTGAAAGCTGTCGCGTTCACAGAGGAACAAGCCCCC	1800

QY 1801 CAGCTGAGGGGCTGTGTGAATCGACACAGCCTCCAGCAGAGGTGTGGAGCTGCAGCTGA 1860
 Db 1801 CAGCTGAGGGGCTGTGTGAATCGACACAGCCTCCAGCAGAGGTGTGGAGCTGCAGCTGA 1860
 QY 1861 GGGGAAGAGACAAATCGGCTGACACTCAGAGGGGTCAAAAGGAGACTTTGGTCGCACC 1920
 Db 1861 GGGGAAGAGACAAATCGGCTGACACTCAGAGGGGTCAAAAGGAGACTTTGGTCGCACC 1920
 QY 1921 ACTCATCTGCGACACCCCGAGAAATGCATCCTGCTCATCAGGTCCAGATTTCTTCCAAAG 1980
 Db 1921 ACTCATCTGCGACACCCCGAGAAATGCATCCTGCTCATCAGGTCCAGATTTCTTCCAAAG 1980
 QY 1981 CGGAGCTTTCTGTGGAAATCTTAGTCTTGGCTCGGACACTTCTTCTGTAGCTGG 2040
 Db 1981 CGGAGCTTTCTGTGGAAATCTTAGTCTTGGCTCGGACACTTCTTCTGTAGCTGG 2040
 QY 2041 GGAGTGTGTGAGGCGAGTGAAGAGGCGGATGGTCACTCAGATCCACAGAGCCCA 2100
 Db 2041 GGAGTGTGTGAGGCGAGTGAAGAGGCGGATGGTCACTCAGATCCACAGAGCCCA 2100
 QY 2101 GGATCAAGGAGACCACTGAGTGCGAGGACAGTGTGGGCCCCCAGCCCAACCTGCAC 2160
 Db 2101 GGATCAAGGAGACCACTGAGTGCGAGGACAGTGTGGGCCCCCAGCCCAACCTGCAC 2160
 QY 2161 AGCCTCATCCCTCTTGGCTTGAGCGGTGAGGCGCTGTGCTGAGTGTCTGACCCGAGA 2220
 Db 2161 AGCCTCATCCCTCTTGGCTTGAGCGGTGAGGCGCTGTGCTGAGTGTCTGACCCGAGA 2220
 QY 2221 CACTCACAGCTTTGTCTATCAGGCGACAGGCTTCTCGAGCGAGGATGATCTGCGCACG 2280
 Db 2221 CACTCACAGCTTTGTCTATCAGGCGACAGGCTTCTCGAGCGAGGATGATCTGCGCACG 2280
 QY 2281 CTTGGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
 Db 2281 CTTGGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
 QY 2341 CTGCACAGTATGTAGTTACCAAGAAATAAAGCGCAATAATTGAGAAAAAAA 2395
 Db 2341 CTGCACAGTATGTAGTTACCAAGAAATAAAGCGCAATAATTGAGAAAAAAA 2395

RESULT 10
 US-10-063-563-139
 ; Sequence 139, Application US/10063563
 ; Publication No. US20030060602A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,563
 ; CURRENT FILING DATE: 2002-05-02
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 139
 ; LENGTH: 2395
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-063-563-139

Query Match 100.0%; Score 2395; DB 13; Length 2395;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGAGCCGGAAGCGCGCTGCAGACGAGCGAGGTCTCAGGTGGGTGCGTTCGCGATC 60
 Db 1 CCTGGAGCCGGAAGCGCGCTGCAGACGAGCGAGGTCTCAGGTGGGTGCGTTCGCGATC 60
 QY 61 CAGCTTAGCTGTCCAGATGCGGCTGGCTCCGGGACTTTCGCTACTCTGTGCGTAGCG 120
 Db 61 CAGCTTAGCTGTCCAGATGCGGCTGGCTCCGGGACTTTCGCTACTCTGTGCGTAGCG 120
 QY 121 ATCGAGGTGTAGGGATCGCGGTCTTCTTCCGGGATTTCTTCCGGGTCTCCGTTCTGTTCC 180
 Db 121 ATCGAGGTGTAGGGATCGCGGTCTTCTTCCGGGATTTCTTCCGGGTCTCCGTTCTGTTCC 180
 QY 181 TCTGCCAGAGCGGAACACGAGCGAGCGGCCCGGAGCCCGGAGCCCGGAGCCCGAGT 240
 Db 181 TCTGCCAGAGCGGAACACGAGCGAGCGGCCCGGAGCCCGGAGCCCGGAGCCCGAGT 240
 QY 241 TCTAACTGGACCGCTGCCACCACTCTCTTCAAGGGTGTGAAATTTATGTTCTCATAGAT 300
 Db 241 TCTAACTGGACCGCTGCCACCACTCTCTTCAAGGGTGTGAAATTTATGTTCTCATAGAT 300
 QY 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAGGGTGTGAAATTTATGTTCTCATAGAT 360
 Db 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAGGGTGTGAAATTTATGTTCTCATAGAT 360
 QY 361 TACCTTGAGAAAAGAGAGATCTCAGATTTTGTGCTGAGCAAGCAAGCCACCTACAGTT 420
 Db 361 TACCTTGAGAAAAGAGAGATCTCAGATTTTGTGCTGAGCAAGCAAGCCACCTACAGTT 420
 QY 421 ACTATGCTCGAATCAAGGCAATGATGACGGGGAGCCTTCTGCTTGTGCGAGTCAATC 480
 Db 421 ACTATGCTCGAATCAAGGCAATGATGACGGGGAGCCTTCTGCTTGTGCGAGTCAATC 480
 QY 481 AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGCAAGCAAGCAAGT 540
 Db 481 AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGCAAGCAAGCAAGT 540
 QY 541 GGAAAAAGATAGTCTTTTATGAGATGAAACCTGGGTGAAATTTATTTCCAAAGCATTTT 600
 Db 541 GGAAAAAGATAGTCTTTTATGAGATGAAACCTGGGTGAAATTTATTTCCAAAGCATTTT 600
 QY 601 GTGGAATATGATGAAACCACTCTTCTGTCAGATTTTCTGTCAGATTTACAGAGTGTGATAAT 660
 Db 601 GTGGAATATGATGAAACCACTCTTCTGTCAGATTTTCTGTCAGATTTACAGAGTGTGATAAT 660
 QY 661 GTCACGAGCATTTGGATTAAGATTTAAAAAGAGAGATTTGGACATATTAATCTCCAC 720
 Db 661 GTCACGAGCATTTGGATTAAGATTTAAAAAGAGAGATTTGGACATATTAATCTCCAC 720
 QY 721 TACCTGGGCTGGACCATTTGGCCACATTTTGGGGCCCAACAGCCCTGATTTGGGAG 780
 Db 721 TACCTGGGCTGGACCATTTGGCCACATTTTGGGGCCCAACAGCCCTGATTTGGGAG 780
 QY 781 AAGCTGAGCGAGATGAGCAGCGTGTGATGAAGATCCACACTCACTGAGTTCGAGGAG 840
 Db 781 AAGCTGAGCGAGATGAGCAGCGTGTGATGAAGATCCACACTCACTGAGTTCGAGGAG 840
 QY 841 AGAGAGACGCTTTTACCCAAATTTGCTGTTCTTGTGTTGACCATGAGGATGTCGAAACA 900
 Db 841 AGAGAGACGCTTTTACCCAAATTTGCTGTTCTTGTGTTGACCATGAGGATGTCGAAACA 900
 QY 901 GGAAGTACGGGGCTCTTCCACCGAGGAGTGAATACCTCTCATTTTATCATGTTCT 960
 Db 901 GGAAGTACGGGGCTCTTCCACCGAGGAGTGAATACCTCTCATTTTATCATGTTCT 960
 QY 961 GCGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGCAGTCCAAATAGCGATGTG 1020
 Db 961 GCGTTTGAAGGAAACCCGGTGATATCCGACATCCAAAGCAGTCCAAATAGCGATGTG 1020
 QY 1021 GCTGCGACACTGCGGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGAGCCTC 1080
 Db 1021 GCTGCGACACTGCGGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGAGCCTC 1080
 QY 1081 CTAATTTCCCAAGTGTGGAAGGAGAACCAATGAGAGAGAGTGTGAGATTTTATCATTTGAAT 1140


```
; APPLICANT: Watanabe Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,553
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 139
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-553-139

Query Match      100.0%; Score 2395; DB 13; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGAGCGGAGCGGGCTGCGAGCAGGCGGAGGCTCCAGGTGGGTCCGGATC 60
Db 1 CCTGGAGCGGAGCGGGCTGCGAGCAGGCGGAGGCTCCAGGTGGGTCCGGATC 60
QY 61 CAGCCTAGCGTGTCCACGATGCGGCTCGGCTCCGGACTTTTCGCTACCTGTTGGTAGCG 120
Db 61 CAGCCTAGCGTGTCCACGATGCGGCTCGGCTCCGGACTTTTCGCTACCTGTTGGTAGCG 120
QY 121 ATCAGGTGCTAGGAPCGGGTCTTCTTCGGGGATTCTTCCGGGCTCCGGTTCGTTCC 180
Db 121 ATCAGGTGCTAGGATCGCGGTCTTCTTCGGGGATTCTTCCGGGCTCCGGTTCGTTCC 180
QY 181 TCTGCCAGAGCGGACACGAGCGGAGCGGCCCGCAGCGCCGGAACCTCGGCTGGAGCCAGT 240
Db 181 TCTGCCAGAGCGGAAACACGAGCGGAGCGGCCCGCAGCGCCGGAACCTCGGCTGGAGCCAGT 240
QY 241 TCTAACTGGACACCGCTGCCACCACTCTCTTCAGTAAAGTTGTTATTTCTGATAGAT 300
Db 241 TCTAACTGGACACCGCTGCCACCACTCTCTTCAGTAAAGTTGTTATTTCTGATAGAT 300
QY 301 GCCTTGAGAGATGATTTGTTGGTCAAGGGTGTGAAATTTATGCCCTACACAAC 360
Db 301 GCCTTGAGAGATGATTTGTTGGTCAAGGGTGTGAAATTTATGCCCTACACAAC 360
QY 361 TACCTGTGAAAAGAGGAGCATCTCAGATTTTGTGCTGAAGCAAGCAACCTACAGTT 420
Db 361 TACCTGTGAAAAGAGGAGCATCTCAGATTTTGTGCTGAAGCAAGCAACCTACAGTT 420
QY 421 ACTATGCTCGAATCAAGGCAATGATGACGGGAGCGCTTCTGGCTTTGTCGAGTCATC 480
Db 421 ACTATGCTCGAATCAAGGCAATGATGACGGGAGCGCTTCTGGCTTTGTCGAGTCATC 480
QY 481 AGGAACTCAATTTCTCTGCACTGTGGAAGACAGTGTGATGACAAAGCAAGCAAGT 540
Db 481 AGGAACTCAATTTCTCTGCACTGTGGAAGACAGTGTGATGACAAAGCAAGCAAGT 540
QY 541 GGAAGAGATAGCTTTTATGAGATGAACCTGGGTAAATTTATTTCCCAAGCAATTT 600
Db 541 GGAAGAGATAGCTTTTATGAGATGAACCTGGGTAAATTTATTTCCCAAGCAATTT 600
QY 601 GTGGAATATGATGGAAACAACTCATTTTTCGTGTGATGATGACAGAGTGGATATAAT 660
Db 601 GTGGAATATGATGGAAACAACTCATTTTTCGTGTGATGATGACAGAGTGGATATAAT 660
QY 661 GTCAGGAGCATTTGGATAAGTATTAAGAGGAGATTGGGACATATTAATCTCCAC 720
Db 661 GTCAGGAGCATTTGGATAAGTATTAAGAGGAGATTGGGACATATTAATCTCCAC 720
QY 721 TACCTGGGCTGACACATTTGSCCATTTTACGGGCCCAACGCCCTGATTTGGGAG 780
Db 721 TACCTGGGCTGACACATTTGSCCATTTTACGGGCCCAACGCCCTGATTTGGGAG 780
QY 781 AAGCTGAGGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAAGTGGAGGAG 840
Db 781 AAGCTGAGGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAAGTGGAGGAG 840
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Db 781 AAGCTGAGGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAAGTGGAGGAG 840
QY 841 AGAGAGACGCGCTTTTACCCAAATTTCTGGTCTTTTGTGTGACCATGGCATCTCTGAACA 900
Db 841 AGAGAGACGCGCTTTTACCCAAATTTCTGGTCTTTTGTGTGACCATGGCATCTCTGAACA 900
QY 901 GGAAGTCAAGGGGCTCTCTCCACGAGGAGTGAATACACCTCTGATTTTAAATCAGTTCT 960
Db 901 GGAAGTCAAGGGGCTCTCTCCACGAGGAGTGAATACACCTCTGATTTTAAATCAGTTCT 960
QY 961 GCGTTTCAGAGGAAACCCGGTGTATCCGACATCCAAAGCACAGTGTAGGAGCGCTC 1020
Db 961 GCGTTTCAGAGGAAACCCGGTGTATCCGACATCCAAAGCACAGTGTAGGAGCGCTC 1020
QY 1021 GCTGCGACACTGCGGATAGCACTTTGGCTTACCGATTCCAAAGACAGTGTAGGAGCGCTC 1080
Db 1021 GCTGCGACACTGCGGATAGCACTTTGGCTTACCGATTCCAAAGACAGTGTAGGAGCGCTC 1080
QY 1081 CTATTTCCAGTTGTGGAAGAACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
Db 1081 CTATTTCCAGTTGTGGAAGAACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
QY 1141 ACAGTGACAGCTTAGTAAACTGTTGCAAGAGATGTCGCGTCATATGAAAAGATCCTGGG 1200
Db 1141 ACAGTGACAGCTTAGTAAACTGTTGCAAGAGATGTCGCGTCATATGAAAAGATCCTGGG 1200
QY 1201 TTTGAGCAGTTTAAATGTGCAAGAGATGTCGGAACCTGGATCGACATGTACTTGGAG 1260
Db 1201 TTTGAGCAGTTTAAATGTGCAAGAGATGTCGGAACCTGGATCGACATGTACTTGGAG 1260
QY 1261 GAAAAGCAATTCAGAGTCTTATTAACCTGGGCTCAAGGTTCTTCAGGAGTACCTGGAT 1320
Db 1261 GAAAAGCAATTCAGAGTCTTATTAACCTGGGCTCAAGGTTCTTCAGGAGTACCTGGAT 1320
QY 1321 GCTCTGAGAGCGTGTAGCTTGTCCCTGAGTGCACAGTGGCCCCAGTTCTCACCTGCTCC 1380
Db 1321 GCTCTGAGAGCGTGTAGCTTGTCCCTGAGTGCACAGTGGCCCCAGTTCTCACCTGCTCC 1380
QY 1381 TGCTCAGCGTTCACACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACTGTCACTC 1440
Db 1381 TGCTCAGCGTTCACACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACTGTCACTC 1440
QY 1441 CTGGGTTTCTCTGCTCTTTTATTTGGTGTCTGTTCTTTTGGCGGCTTCAGTCAATG 1500
Db 1441 CTGGGTTTCTCTGCTCTTTTATTTGGTGTCTGTTCTTTTGGCGGCTTCAGTCAATG 1500
QY 1501 TGTGCACTCAGCTGAAAGTTGCTGTACTTCTGTGSCCTCTGCTGCGCGGAGGCT 1560
Db 1501 TGTGCACTCAGCTGAAAGTTGCTGTACTTCTGTGSCCTCTGCTGCGCGGAGGCT 1560
QY 1561 GCCTTTTCTGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCT 1620
Db 1561 GCCTTTTCTGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCT 1620
QY 1621 TGACAGGCGGCTCAGGAGAGCACTGTGAGAGCAGCTTATCCAGGCTCTGGGTGTCC 1680
Db 1621 TGACAGGCGGCTCAGGAGAGCACTGTGAGAGCAGCTTATCCAGGCTCTGGGTGTCC 1680
QY 1681 GACACAGGTTTTCACATCTGTGCTGTGTCAGTCAAGTGCCTCAGTTCTTGGAAGCTAGGT 1740
Db 1681 GACACAGGTTTTCACATCTGTGCTGTGTCAGTCAAGTGCCTCAGTTCTTGGAAGCTAGGT 1740
QY 1741 TCTGCGACTGTTTACCAAGTGTATTTAAAGAGCTGCGGCTCAAGAGGAAACAGGCCCTC 1800
Db 1741 TCTGCGACTGTTTACCAAGTGTATTTAAAGAGCTGCGGCTCAAGAGGAAACAGGCCCTC 1800
QY 1801 CAGCTGAGGGGTGTGTGAATCGGACAGCTTCCAGAGAGGTTGTGGAGCTGCAGCTGA 1860
Db 1801 CAGCTGAGGGGTGTGTGAATCGGACAGCTTCCAGAGAGGTTGTGGAGCTGCAGCTGA 1860
QY 1861 GGAAGAGAGCAATTCGGCTGGACACTCAGAGAGGTTCAAGAGGAGCTTGGTGCAC 1920
Db 1861 GGAAGAGAGCAATTCGGCTGGACACTCAGAGAGGTTCAAGAGGAGCTTGGTGCAC 1920
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1921 ACTATCTCTCCACCCAGATGATGATCTCTGCTCATCAGGTCAGATTTCTTCCAAAG 1980
1921 ACTCATCTCCACCCAGATGATGATCTCTGCTCATCAGGTCAGATTTCTTCCAAAG 1980
1981 CGGAGCTTTTCTGTTGGAATTTCTAGTCTTGGCTCGGACACCTTCAATTCGTTAGCTGG 2040
1981 CGGAGCTTTTCTGTTGGAATTTCTAGTCTTGGCTCGGACACCTTCAATTCGTTAGCTGG 2040
2041 GGAGTGTGTGAGGCGAGTGAAGAAGAGGCGGATGGTCACTCAGATCCACAGAGCCCA 2100
2041 GGAGTGTGTGAGGCGAGTGAAGAAGAGGCGGATGGTCACTCAGATCCACAGAGCCCA 2100
2101 GGATCAAGGAGCCACCTGCTGAGTGCAGCAGACGATTTGGGCCCCCACCACCCCTGCAC 2160
2101 GGATCAAGGAGCCACCTGCTGAGTGCAGCAGACGATTTGGGCCCCCACCACCCCTGCAC 2160
2161 AGCCTCATCCCTCTTGGCTTGGCTGAGCGCTCAGAGCCCTGTGCTGAGTGTCTGACCGAGA 2220
2161 AGCCTCATCCCTCTTGGCTTGGCTGAGCGCTCAGAGCCCTGTGCTGAGTGTCTGACCGAGA 2220
2221 CACTCACAGCTTTGTCATCAGGCGACAGGCTTCTCGGAGCGAGATGATCTGTGCGCAGG 2280
2221 CACTCACAGCTTTGTCATCAGGCGACAGGCTTCTCGGAGCGAGATGATCTGTGCGCAGG 2280
2281 CTTGCACTCGGCGCCATCTGGCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
2281 CTTGCACTCGGCGCCATCTGGCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
2341 CTGCACAGATGTAGTTTACCAAGAATAAAGCGCAATTAATGAGAAAAAAA 2395
2341 CTGCACAGATGTAGTTTACCAAGAATAAAGCGCAATTAATGAGAAAAAAA 2395

RESULT 13
US-10-063-554-139
; Sequence 139, Application US/10063554
; Publication No. US20030040013A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,554
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 139
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-554-139

Query Match 100.0%; Score 2395; DB 13; Length 2395;
Best Local Similarity 100.0%; Pred No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGAGCGCGAGCGCGCTGCGAGCGGCGAGGCTCAGGTGGGTCGGTTCGCGATC 60
DB 1 CCTGAGCGCGAGCGCGCTGCGAGCGGCGAGGCTCAGGTGGGTCGGTTCGCGATC 60
QY 61 CAGCCTAGGCTGCCAGGATCGGCTGGGCTCGGACCTTCGCTACCTGTTGCGTAGCG 120
DB 61 CAGCCTAGGCTGCCAGGATCGGCTGGGCTCGGACCTTCGCTACCTGTTGCGTAGCG 120

121 ATCGAGTGTAGGATCGCGGTCTTCTTCCGGGATTTCTTCCGGCTCCGTTCTGTTCC 180
121 ATCGAGTGTAGGATCGCGGTCTTCTTCCGGGATTTCTTCCGGCTCCGTTCTGTTCC 180
181 TCTGCCAGAGCGGAAACACGAGCGGAGCCCGCCAGCGCCGAAACCCCTCGGTGAGCCAGT 240
181 TCTGCCAGAGCGGAAACACGAGCGGAGCCCGCCAGCGCCGAAACCCCTCGGTGAGCCAGT 240
241 TCTAACTGGACACCGCTGCCACACCTCTCTTTCAGTAAAGTTGTTATTTGTTCTGATAGT 300
241 TCTAACTGGACACCGCTGCCACACCTCTCTTTCAGTAAAGTTGTTATTTGTTCTGATAGT 300
301 GCCTTGAGAGATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 360
301 GCCTTGAGAGATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 360
361 TACCTTGTGAAAGAGAGATCTCAGATTTTCTGCTGAGGAGCCCTTCTGCTTGTGCGATC 420
361 TACCTTGTGAAAGAGAGATCTCAGATTTTCTGCTGAGGAGCCCTTCTGCTTGTGCGATC 420
421 ACTATGCTCGAATCAAGGCAATTCATGACGGGAGCCCTTCTGCTTGTGCGATC 480
421 ACTATGCTCGAATCAAGGCAATTCATGACGGGAGCCCTTCTGCTTGTGCGATC 480
481 AGGAACCTCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
481 AGGAACCTCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
541 GGAAGAGATGATGTTTATGAGAGTGAACCTGGGTTAAATTTATTTCCAAAGCATTTT 600
541 GGAAGAGATGATGTTTATGAGAGTGAACCTGGGTTAAATTTATTTCCAAAGCATTTT 600
601 GTGCAATATGATGAAACAACTCTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
601 GTGCAATATGATGAAACAACTCTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
661 GTGCAAGGCAATTTGGATAAAGTATTAAGAGAGAGATTTGGGACATATTAATCTCCAC 720
661 GTGCAAGGCAATTTGGATAAAGTATTAAGAGAGAGATTTGGGACATATTAATCTCCAC 720
721 TACCTGGGCTGGACCAATTTGGGACCAATTTTCCAGGCGCCCAACAGCCCTGATTTGGGAG 780
721 TACCTGGGCTGGACCAATTTGGGACCAATTTTCCAGGCGCCCAACAGCCCTGATTTGGGAG 780
781 AAGCTGAGCGAGATGAGACAGCGTCTGATGAAGATCCACCTCCTCAGTCTGAGGAG 840
781 AAGCTGAGCGAGATGAGACAGCGTCTGATGAAGATCCACCTCCTCAGTCTGAGGAG 840
841 AGAGAGCGCTTTACCAATTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 900
841 AGAGAGCGCTTTTACCAATTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 900
901 GGAAGTCAAGGCGCTTCTTCCACCGAGGAGTGAATACACCTCTGATTTTAAATCAGTTCT 960
901 GGAAGTCAAGGCGCTTCTTCCACCGAGGAGTGAATACACCTCTGATTTTAAATCAGTTCT 960
961 GCGTTTGAAGGAAACCCCGGTGATATCCACATCCAAAGCACTCCAAAGCAGTCCAAATAGCGATG 1020
961 GCGTTTGAAGGAAACCCCGGTGATATCCACATCCAAAGCAGTCCAAATAGCGATG 1020
1021 GCTGGACACTGCGGATAGCACTTGGCTTACCGATTCCAAAGAGAGAGTGTAGGAGCCCTC 1080
1021 GCTGGACACTGCGGATAGCACTTGGCTTACCGATTCCAAAGAGAGAGTGTAGGAGCCCTC 1080
1081 CTATTTCCCAAGTTGTGGAAG 1140
1081 CTATTTCCCAAGTTGTGGAAG 1140
1141 ACAGTCAAGCTTGTAACTGTTGGAAG 1200
1141 ACAGTCAAGCTTGTAACTGTTGGAAG 1200
1201 TTTGAGCAGCTTTTAAATGTGAG 1260

RESULT 15
US-10-305-654-291
; Sequence 291, Application US/10305654
; Publication No. US20030224984A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrera, Napoleone
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Paoni, J.
; APPLICANT: Paoni, N. F.
; APPLICANT: Stephan, J-P F.
; APPLICANT: Watanabe, C.K.
; APPLICANT: Wood, W.I.
; APPLICANT: Williams, P.M.
; APPLICANT: Ye, Wellan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235R1C1
; CURRENT APPLICATION NUMBER: US/10/305,654
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 291
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homosapiens
US-10-305-654-291

Query Match 100.0%; Score 2395; DB 13; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CCTGGAGCGGAGCGGCTGCGAGCGGAGCGGCTCCAGTGGGGTTCGGATC	60
DB	1	CCTGGAGCGGAGCGGCTGCGAGCGGAGCGGCTCCAGTGGGGTTCGGATC	60
QY	61	CAGCTAGCGTGCACGATCGCGCTCGGCTCGGAGCTTCCTCCGGCTCCCGTTC	120
DB	61	CAGCTAGCGTGCACGATCGCGCTCGGCTCGGAGCTTCCTCCGGCTCCCGTTC	120
QY	121	ATCGAGTGTAGGATCGCGCTTCCTTCGGGGATTCTTCGGGGTCCCGTTCGTTCC	180
DB	121	ATCGAGTGTAGGATCGCGCTTCCTTCGGGGATTCTTCGGGGTCCCGTTCGTTCC	180
QY	181	TCGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG	240
DB	181	TCGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG	240
QY	241	TCTAATGACGACCGCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG	300
DB	241	TCTAATGACGACCGCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG	300
QY	301	GCCTTGAGAGATGATTTGTTGGTCAAGGGTGTGAAATTTATGCGCTTACAACT	360
DB	301	GCCTTGAGAGATGATTTGTTGGTCAAGGGTGTGAAATTTATGCGCTTACAACT	360
QY	361	TACCTTGTGAAAGAGGAGCATCTACAGTTTGTGGCTGAAGCAAGCACTACAGTT	420
DB	361	TACCTTGTGAAAGAGGAGCATCTACAGTTTGTGGCTGAAGCAAGCACTACAGTT	420
QY	421	ACTATGCTCGAATCAAGCATTCAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG	480
DB	421	ACTATGCTCGAATCAAGCATTCAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG	480
QY	481	AGGAACCTCAATTCCTCGACTGCTGGAAGACAGTGTGATAGACAAGCAAGCAGCT	540
DB	481	AGGAACCTCAATTCCTCGACTGCTGGAAGACAGTGTGATAGACAAGCAAGCAGCT	540

Db	481	AGGAACCTCAATTCCTCGACTGCTGGAAGACAGTGTGATAGACAAGCAAGCAGCT	540
QY	541	CGAAAAAGAAATAGTCTTTTATGAGATGAACCTGGTGAATATTTCCCAAGCAATTT	600
Db	541	CGAAAAAGAAATAGTCTTTTATGAGATGAACCTGGTGAATATTTCCCAAGCAATTT	600
QY	601	GTGGAATATGATGGAACCACTCATTTTCGTGTGATTAACACAGAGGTGATATAAT	660
Db	601	GTGGAATATGATGGAACCACTCATTTTCGTGTGATTAACACAGAGGTGATATAAT	660
QY	661	GTGAGAGCGCATTTGATTAAGTATTAAGAGAGGATTTGGACATATTAATCTCCAC	720
Db	661	GTGAGAGCGCATTTGATTAAGTATTAAGAGAGGATTTGGACATATTAATCTCCAC	720
QY	721	TACCTGGGCTGGACCACTTTCAGGGCCCAAGAGCGGCTGATTTGGGAG	780
Db	721	TACCTGGGCTGGACCACTTTCAGGGCCCAAGAGCGGCTGATTTGGGAG	780
QY	781	AGCTGAGCGAGATGAGACAGCGTGTGATGAAGATCCACACCTCACTGAGTCGAGAG	840
Db	781	AGCTGAGCGAGATGAGACAGCGTGTGATGAAGATCCACACCTCACTGAGTCGAGAG	840
QY	841	AGAGAGCGCTTTACCAATTTGCTGTTCTTTGTGGTACCAATGATGCTGCTGCTG	900
Db	841	AGAGAGCGCTTTACCAATTTGCTGTTCTTTGTGGTACCAATGATGCTGCTGCTG	900
QY	901	GGAAGTCAAGGGCTCTCCACGAGGAGTGAATACACCTGATTTTAACTGATTTCT	960
Db	901	GGAAGTCAAGGGCTCTCCACGAGGAGTGAATACACCTGATTTTAACTGATTTCT	960
QY	961	CGCTTTGAAAGGAAACCGGCTGATATCCGACATCCAAAGCAGCTCCATAGACGATG	1020
Db	961	CGCTTTGAAAGGAAACCGGCTGATATCCGACATCCAAAGCAGCTCCATAGACGATG	1020
QY	1021	GCTCGGACACTGGGATAGACTTGGCTTACCGATTCGAAAGACAGTGTGAGGAGCTC	1080
Db	1021	GCTCGGACACTGGGATAGACTTGGCTTACCGATTCGAAAGACAGTGTGAGGAGCTC	1080
QY	1081	CTATTTCCAGTTGTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1140
Db	1081	CTATTTCCAGTTGTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1140
QY	1141	ACAGTCAAGCTTAACTGTTGCAAGAGATGCGCTCATATGAAAGAGTCTCTGGG	1200
Db	1141	ACAGTCAAGCTTAACTGTTGCAAGAGATGCGCTCATATGAAAGAGTCTCTGGG	1200
QY	1201	TTTGAGCAGTTTAAATGTGCAAGAGATGCGATGGGAACTGGATCAGATGCTGGAG	1260
Db	1201	TTTGAGCAGTTTAAATGTGCAAGAGATGCGATGGGAACTGGATCAGATGCTGGAG	1260
QY	1261	GAAAGCAATTCAGAGTCTTATTCAGCTGGCTTCAAGGTTCTCAGGAGTACCTGGAT	1320
Db	1261	GAAAGCAATTCAGAGTCTTATTCAGCTGGCTTCAAGGTTCTCAGGAGTACCTGGAT	1320
QY	1321	GCTCTGAAGCGCTGAGTGTCTTCCAGTGCACAGTGGGCTTCTCAGCTGCTCC	1380
Db	1321	GCTCTGAAGCGCTGAGTGTCTTCCAGTGCACAGTGGGCTTCTCAGCTGCTCC	1380
QY	1381	TGCTCAGCGTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1440
Db	1381	TGCTCAGCGTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1440
QY	1441	CTGGGTTTCTCTGCTCTTTTATTTGTTGATCTGTTCTTTTCGGCGTTTCTGATG	1500
Db	1441	CTGGGTTTCTCTGCTCTTTTATTTGTTGATCTGTTCTTTTCGGCGTTTCTGATG	1500
QY	1501	TGTGACCTCAGTGAAGTGTGCTACTTCTGTGGCTCTGTGGCTGGGCGGAGGCT	1560
Db	1501	TGTGACCTCAGTGAAGTGTGCTACTTCTGTGGCTCTGTGGCTGGGCGGAGGCT	1560
QY	1561	GCCTTTGTTTACGAGCTCTGTTGAACACCTGTTGTGCGAAGTGTGCGAGTGCCT	1620
Db	1561	GCCTTTGTTTACGAGCTCTGTTGAACACCTGTTGTGCGAAGTGTGCGAGTGCCT	1620

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QY	1621	TGGACAGGGGGCTCAGGGAAGCACTGTGAGCAGCGCTTATCCCAAGGCTCTGGGTGTCCC	1680
Db	1621		1680
QY	1681	GACACAGGTGTTACACATCTGTCTGTCTCAGGTGAGATGCTCTGATCTTTGGAAAGCTAGGT	1740
Db	1681		1740
QY	1741	TCCTGGGACATGTTTACCAAGGTGATTTGAAGAGCTGGGGTCCACAGAGGAAACAAGCCCCC	1800
Db	1741		1800
QY	1801	CAGCTGAGGGGTGTGTGAATCCGACAGGCTCTCCAGCAGAGGTGTGGAGCTGTGAGCTGA	1860
Db	1801		1860
QY	1861	GGGAAGAGAGACAATCGGCTCGGACACTCAGAGAGGTCAAAGAGAGACTTGGTCGCACC	1920
Db	1861		1920
QY	1921	ACTCATCTCGCACCCCGAAGTCATCTCTGCCTCATCAGTCCAGATTTCTTTCCAAAG	1980
Db	1921		1980
QY	1981	CGGAGCTTTTCTGTTGGAAATCTTAGTCTTGGCTCGGACACCTTCACTCGCTTAGCTGG	2040
Db	1981		2040
QY	2041	GGAGTGTGTGAGGCAGTGAAGAGAGGCGGATGTGCACACTCAGATCCACAGAGGCCA	2100
Db	2041		2100
QY	2101	GGATCAAGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCGCCAACCCCTGCAC	2160
Db	2101		2160
QY	2161	AGCCCTCATCCCTCTTGGCTTGAGCCGTGAGAGCCCTGTGTGAGTGTCACACGAGA	2220
Db	2161		2220
QY	2221	CACTCAGACTTTGTCAATCAGGACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACG	2280
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QY	2281	CTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGATTTGAATTAGTACCTAG	2340
Db	2281		2340
QY	2341	CTGCACAGTATGTATTACAAAGAAATAAAGCGCAATAATTGAGAAAAAAA	2395
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Search completed: August 5, 2004, 22:54:35
Job time : 1097 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	53	2.2	578	4	US-09-621-976-252	Sequence 252, Appl	
2	42	1.8	7218	1	US-08-232-463-14	Sequence 14, Appl	
3	39.6	1.7	7218	1	US-08-232-463-14	Sequence 14, Appl	
C	38.8	1.6	832	4	US-09-621-976-2813	Sequence 2813, Ap	
4	37.4	1.6	2527	4	US-09-555-790A-1	Sequence 1, Appli	
C	37	1.5	458	3	US-09-141-000-4	Sequence 4, Appli	
6	37	1.5	505	4	US-09-621-976-15639	Sequence 15639, A	
7	36.8	1.5	969	4	US-09-488-039A-2802	Sequence 2802, Ap	
8	36.8	1.5	1033	4	US-09-610-185C-3	Sequence 3, Appli	
9	36.6	1.5	364	4	US-09-621-976-17202	Sequence 17202, A	
10	36.6	1.5	2480	4	US-09-023-655-1096	Sequence 1096, Ap	
C	36.2	1.5	77536	4	US-09-410-551B-1	Sequence 1, Appli	
C	35.4	1.5	17000	4	US-09-678-299A-18	Sequence 18, Appl	
13	35.4	1.5	118067	4	US-09-497-855A-32	Sequence 32, Appl	
C	35.2	1.5	444	4	US-08-252-921A-12919	Sequence 12919, A	
16	35.2	1.5	882	4	US-09-252-991A-12566	Sequence 12566, A	
C	35.2	1.5	918	4	US-08-956-171E-513	Sequence 513, App	
17	35.2	1.5	918	4	US-08-956-171E-513	Sequence 1240, A	
C	35.2	1.5	1422	4	US-09-252-991A-13240	Sequence 13065, A	
19	35.2	1.5	1422	4	US-09-252-991A-13065	Sequence 12874, A	
C	35.2	1.5	1485	4	US-09-252-991A-12874	Sequence 1448, Ap	
21	35.2	1.5	1528	4	US-09-016-434-1448	Sequence 7, Appli	
22	35.2	1.5	1659	1	US-08-333-358-7	Sequence 7, Appli	
23	35.2	1.5	1659	1	US-08-463-694-7	Sequence 7, Appli	
24	35.2	1.5	1659	1	US-08-694-501-7	Sequence 7, Appli	
25	35.2	1.5	3001	4	US-09-539-333D-185	Sequence 185, App	
26	35	1.5	2150	3	US-09-263-023-1	Sequence 1, Appli	
27	35	1.5	2150	4	US-09-471-867-1	Sequence 1, Appli	

c 101	32	1.3	32207	2	US-08-770-379-20	Sequence 20, Appl	174	31.2	1.3	2655	2	US-08-470-566B-26	Sequence 26, Appl
c 102	32	1.3	32207	3	US-08-757-669A-20	Sequence 20, Appl	175	31.2	1.3	2655	2	US-08-469-334-17	Sequence 17, Appl
c 103	32	1.3	32207	4	US-09-230-371A-20	Sequence 17, Appl	176	31.2	1.3	2655	2	US-08-469-334-26	Sequence 26, Appl
c 104	32	1.3	32207	5	US-08-770-379-17	Sequence 17, Appl	177	31.2	1.3	2655	3	US-09-300-529-17	Sequence 26, Appl
c 105	32	1.3	35100	2	US-08-757-669A-17	Sequence 17, Appl	178	31.2	1.3	2655	3	US-09-300-529-26	Sequence 49, Appl
c 106	32	1.3	35100	3	US-08-757-669A-17	Sequence 17, Appl	179	31.2	1.3	4031	1	US-08-471-033-49	Sequence 49, Appl
c 107	32	1.3	35100	4	US-09-230-371A-17	Sequence 17, Appl	180	31.2	1.3	4031	2	US-08-471-044-49	Sequence 49, Appl
c 108	31.8	1.3	580073	4	US-08-545-528D-1	Sequence 1, Appl	181	31.2	1.3	4031	2	US-08-463-483A-49	Sequence 49, Appl
c 109	31.8	1.3	543	4	US-09-134-000C-344	Sequence 14, Appl	182	31.2	1.3	4031	2	US-08-471-046A-49	Sequence 49, Appl
c 110	31.8	1.3	501	4	US-09-641-638-163	Sequence 163, App	183	31.2	1.3	4031	2	US-08-470-566B-49	Sequence 49, Appl
c 111	31.8	1.3	1173	3	US-09-414-010-1	Sequence 1, Appl	184	31.2	1.3	4031	3	US-08-469-334-49	Sequence 49, Appl
c 112	31.8	1.3	1173	4	US-09-812-216-1	Sequence 6262, Ap	185	31.2	1.3	4031	3	US-09-300-529-49	Sequence 49, Appl
c 113	31.8	1.3	1788	4	US-09-489-039A-6262	Sequence 1, Appl	186	31.2	1.3	4079	4	US-09-016-434-1246	Sequence 1246, Ap
c 114	31.8	1.3	5727	4	US-09-628-188A-1	Sequence 1, Appl	187	31.2	1.3	4141	4	US-09-245-281-42	Sequence 42, Appl
c 115	31.8	1.3	49272	1	US-08-614-770A-1	Sequence 1, Appl	188	31.2	1.3	4141	4	US-09-207-359B-42	Sequence 42, Appl
c 116	31.6	1.3	430	4	US-09-621-976-16656	Sequence 1656, A	189	31.2	1.3	4141	4	US-09-340-620A-42	Sequence 42, Appl
c 117	31.6	1.3	582	4	US-09-010-147B-13	Sequence 13, Appl	190	31.2	1.3	4141	4	US-09-865-364-42	Sequence 42, Appl
c 118	31.6	1.3	584	4	US-09-671-317-251	Sequence 251, App	191	31.2	1.3	4242	4	US-09-023-655-1201	Sequence 1201, Ap
c 119	31.6	1.3	2235	4	US-09-484-970B-28	Sequence 28, Appl	192	31.2	1.3	4796	3	US-09-085-199B-3	Sequence 3, Appl
c 120	31.6	1.3	2243	4	US-09-620-312D-12	Sequence 12, Appl	193	31.2	1.3	11558	5	PCT-US93-06251-23	Sequence 23, Appl
c 121	31.6	1.3	3306	4	US-09-081-385-10	Sequence 10, Appl	194	31.2	1.3	29629	4	US-09-729-999-3	Sequence 3, Appl
c 122	31.6	1.3	9464	4	US-09-593-580B-1	Sequence 2, Appl	195	31.2	1.3	29629	4	US-10-135-689-3	Sequence 29, Appl
c 123	31.4	1.3	294	3	US-08-776-971-2	Sequence 114, App	196	31	1.3	469	3	US-09-085-199B-29	Sequence 29, Appl
c 124	31.4	1.3	380	3	US-08-776-971-114	Sequence 116, App	197	31	1.3	726	4	US-09-252-991A-6538	Sequence 6538, Ap
c 125	31.4	1.3	380	3	US-08-776-971-116	Sequence 116, App	198	31	1.3	852	4	US-09-252-991A-2774	Sequence 2774, Ap
c 126	31.4	1.3	885	4	US-09-134-000C-1319	Sequence 1319, App	199	31	1.3	1521	4	US-09-252-991A-6495	Sequence 6495, Ap
c 127	31.4	1.3	1117	2	US-08-960-022-1	Sequence 1, Appl	200	31	1.3	1575	4	US-09-252-991A-3100	Sequence 3100, Ap
c 128	31.4	1.3	1358	4	US-09-023-655-84	Sequence 84, Appl	201	31	1.3	1956	4	US-09-252-991A-3189	Sequence 3189, Ap
c 129	31.4	1.3	1473	2	US-08-541-033A-25	Sequence 25, Appl	202	31	1.3	3889	4	US-09-484-970B-39	Sequence 39, Appl
c 130	31.4	1.3	1506	2	US-08-828-451-25	Sequence 25, Appl	203	31	1.3	4098	4	US-09-268-866-1	Sequence 1, Appl
c 131	31.4	1.3	1506	2	US-08-828-451-23	Sequence 23, Appl	204	31	1.3	5238	4	US-09-620-312D-351	Sequence 351, App
c 132	31.4	1.3	1506	2	US-08-828-451-23	Sequence 23, Appl	205	31	1.3	7012	4	US-09-620-312D-351	Sequence 351, App
c 133	31.4	1.3	1969	2	US-08-541-033A-7	Sequence 7, Appl	206	31	1.3	8285	4	US-09-221-017B-173	Sequence 3, Appl
c 134	31.4	1.3	1969	2	US-08-828-451-7	Sequence 7, Appl	207	31	1.3	11827	4	US-09-732-025-3	Sequence 3, Appl
c 135	31.4	1.3	2086	2	US-08-541-033A-19	Sequence 19, Appl	208	30.8	1.3	297	4	US-09-739-455-3	Sequence 4438, Ap
c 136	31.4	1.3	2086	2	US-08-828-451-19	Sequence 19, Appl	209	30.8	1.3	581	4	US-09-833-294A-4438	Sequence 907, App
c 137	31.4	1.3	2099	2	US-08-541-033A-3	Sequence 3, Appl	210	30.8	1.3	896	4	US-09-833-294A-4438	Sequence 22, Appl
c 138	31.4	1.3	2137	2	US-08-828-451-3	Sequence 3, Appl	211	30.8	1.3	896	4	US-09-404-879A-22	Sequence 22, Appl
c 139	31.4	1.3	2137	2	US-08-541-033A-18	Sequence 18, Appl	212	30.8	1.3	896	4	US-09-338-933-22	Sequence 22, Appl
c 140	31.4	1.3	2140	2	US-08-828-451-18	Sequence 18, Appl	213	30.8	1.3	896	4	US-09-215-681-22	Sequence 22, Appl
c 141	31.4	1.3	2140	2	US-08-828-451-1	Sequence 1, Appl	214	30.8	1.3	1269	4	US-09-216-003A-22	Sequence 1803, Ap
c 142	31.4	1.3	3117	3	US-08-909-954-3	Sequence 1, Appl	215	30.8	1.3	3226	1	US-09-107-532A-1803	Sequence 11, Appl
c 143	31.4	1.3	43676	3	US-09-632-652A-5	Sequence 3, Appl	216	30.8	1.3	3226	1	US-07-862-021B-11	Sequence 11, Appl
c 144	31.4	1.3	66804	4	US-09-356-952-12	Sequence 3, Appl	217	30.8	1.3	3226	5	US-08-313-288B-11	Sequence 11, Appl
c 145	31.4	1.3	92407	4	US-09-740-041-3	Sequence 5, Appl	218	30.8	1.3	3772	4	PCT-US93-03164-11	Sequence 5, Appl
c 146	31.4	1.3	1164	3	US-09-085-199B-1	Sequence 3, Appl	219	30.8	1.3	3772	4	US-09-962-665-5	Sequence 5, Appl
c 147	31.2	1.3	1331	4	US-09-023-655-579	Sequence 1, Appl	220	30.8	1.3	4032	1	US-09-963-333-5	Sequence 3, Appl
c 148	31.2	1.3	2004	1	US-09-023-655-579	Sequence 579, App	221	30.8	1.3	4032	1	US-08-107-748-3	Sequence 3, Appl
c 149	31.2	1.3	2004	2	US-08-471-033-18	Sequence 18, Appl	222	30.8	1.3	4032	5	US-08-245-809-4	Sequence 23, Appl
c 150	31.2	1.3	2004	2	US-08-471-033-18	Sequence 18, Appl	223	30.8	1.3	10482	4	PCT-US92-01385-3	Sequence 27, Appl
c 151	31.2	1.3	2004	2	US-08-463-483A-18	Sequence 18, Appl	224	30.8	1.3	11131	4	US-09-322-478-23	Sequence 1, Appl
c 152	31.2	1.3	2004	2	US-08-471-046A-18	Sequence 18, Appl	225	30.8	1.3	14507	3	US-08-785-150-1	Sequence 1, Appl
c 153	31.2	1.3	2004	2	US-08-471-046A-18	Sequence 18, Appl	226	30.8	1.3	14507	3	US-09-660-299-1	Sequence 1, Appl
c 154	31.2	1.3	2004	2	US-08-469-334-18	Sequence 18, Appl	227	30.8	1.3	14507	4	US-09-435-377-1	Sequence 1, Appl
c 155	31.2	1.3	2004	2	US-08-469-334-18	Sequence 18, Appl	228	30.8	1.3	14507	4	US-09-973-928-1	Sequence 1, Appl
c 156	31.2	1.3	2310	4	US-09-300-529-18	Sequence 18, Appl	229	30.8	1.3	35524	3	US-08-923-137-1	Sequence 8, Appl
c 157	31.2	1.3	2547	4	US-09-134-000C-1714	Sequence 1714, Ap	230	30.8	1.3	288	1	US-08-157-171-8	Sequence 120, App
c 158	31.2	1.3	2576	1	US-09-765-298A-9	Sequence 9, Appl	231	30.6	1.3	297	3	US-08-776-971-120	Sequence 120, App
c 159	31.2	1.3	2576	1	US-08-471-033-35	Sequence 35, Appl	232	30.6	1.3	297	3	US-08-776-971-121	Sequence 132, App
c 160	31.2	1.3	2576	2	US-08-471-044-35	Sequence 35, Appl	233	30.6	1.3	380	3	US-08-776-971-132	Sequence 132, App
c 161	31.2	1.3	2576	2	US-08-463-483A-35	Sequence 35, Appl	234	30.6	1.3	474	4	US-09-621-976-18033	Sequence 18033, A
c 162	31.2	1.3	2576	2	US-08-471-046A-35	Sequence 35, Appl	235	30.6	1.3	537	4	US-09-252-991A-13469	Sequence 13469, A
c 163	31.2	1.3	2576	2	US-08-470-566B-35	Sequence 35, Appl	236	30.6	1.3	714	4	US-09-489-039A-2720	Sequence 2720, App
c 164	31.2	1.3	2576	3	US-08-469-334-35	Sequence 35, Appl	237	30.6	1.3	769	3	US-08-776-971-118	Sequence 118, App
c 165	31.2	1.3	2576	3	US-09-300-529-35	Sequence 35, Appl	238	30.6	1.3	769	3	US-08-776-971-119	Sequence 2, Appl
c 166	31.2	1.3	2576	3	US-08-471-033-17	Sequence 17, Appl	239	30.6	1.3	1189	2	US-08-450-042A-2	Sequence 109, App
c 167	31.2	1.3	2555	1	US-08-471-033-26	Sequence 26, Appl	240	30.6	1.3	1218	4	US-09-894-844-109	Sequence 3, Appl
c 168	31.2	1.3	2555	2	US-08-471-044-26	Sequence 26, Appl	241	30.6	1.3	1856	3	US-08-157-171-3	Sequence 128, App
c 169	31.2	1.3	2655	2	US-08-463-483A-17	Sequence 17, Appl	242	30.6	1.3	1856	3	US-09-050-159-128	Sequence 3, Appl
c 170	31.2	1.3	2655	2	US-08-463-483A-26	Sequence 26, Appl	243	30.6	1.3	2271	4	US-09-521-521C-3	Sequence 1, Appl
c 171	31.2	1.3	2655	2	US-08-471-046A-17	Sequence 17, Appl	244	30.6	1.3	2271	4	US-09-396-937-1	Sequence 1098, Ap
c 172	31.2	1.3	2655	2	US-08-471-046A-26	Sequence 26, Appl	245	30.6	1.3	3698	4	US-09-976-594-1098	Sequence 1098, Ap
c 173	31.2	1.3	2655	2	US-08-470-566B-17	Sequence 17, Appl	246	30.6	1.3	8802	3	US-08-896-449A-1	Sequence 1, Appl

247	1.3	8802	3	US-09-132-652-1	Sequence 1, Appli	c 320	30	1.3	2409	4	US-09-252-991A-8479	Sequence 8479, Ap	
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249	30.6	1.3	1664976	4	US-08-916-421B-1	Sequence 11602, A	322	30	1.3	3695	1	US-08-203-676-1	Sequence 1, Appli
C 250	30.4	1.3	333	4	US-09-252-991A-11602	Sequence 11602, A	323	30	1.3	3695	2	US-08-822-238-1	Sequence 7, Appli
C 251	30.4	1.3	437	3	US-08-714-918-52	Sequence 52, Appli	C 324	30	1.3	11459	4	US-09-462-136-7	Sequence 35, Appli
C 252	30.4	1.3	437	3	US-09-265-315-52	Sequence 52, Appli	C 325	30	1.3	19250	4	US-08-961-527-35	Sequence 35, Appli
C 253	30.4	1.3	437	3	US-09-265-315-52	Sequence 52, Appli	C 326	30	1.3	87563	4	US-09-453-702B-57	Sequence 57, Appli
C 254	30.4	1.3	437	3	US-09-266-417-52	Sequence 52, Appli	327	30	1.3	112132	4	US-09-741-150-3	Sequence 3, Appli
C 255	30.4	1.3	437	4	US-09-268-709-52	Sequence 52, Appli	328	30	1.3	112132	4	US-10-160-187-3	Sequence 3, Appli
C 256	30.4	1.3	437	3	US-08-933-983-20	Sequence 52, Appli	329	29.8	1.2	289	3	US-09-007-005-17	Sequence 3, Appli
C 257	30.4	1.3	447	3	US-08-933-983-20	Sequence 52, Appli	330	29.8	1.2	289	3	US-09-244-796-17	Sequence 17, Appli
C 258	30.4	1.3	505	4	US-09-621-976-15639	Sequence 15639, A	331	29.8	1.2	423	3	US-09-040-984-61	Sequence 61, Appli
C 259	30.4	1.3	708	4	US-09-328-352-2733	Sequence 2733, Ap	332	29.8	1.2	423	3	US-09-123-913-61	Sequence 61, Appli
C 260	30.4	1.3	786	4	US-09-252-991A-11775	Sequence 11775, A	333	29.8	1.2	423	4	US-09-643-597-61	Sequence 61, Appli
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C 262	30.4	1.3	1358	4	US-09-252-991A-13498	Sequence 13498, A	335	29.8	1.2	423	4	US-09-542-618A-61	Sequence 61, Appli
C 263	30.4	1.3	1257	4	US-09-543-681A-3206	Sequence 3206, Ap	336	29.8	1.2	423	4	US-09-606-421B-61	Sequence 61, Appli
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C 266	30.4	1.3	2351	4	US-09-620-312D-848	Sequence 848, App	339	29.8	1.2	576	4	US-09-540-236-402	Sequence 402, App
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C 273	30.4	1.3	4870	3	US-08-664-962B-7	Sequence 7, Appli	346	29.8	1.2	1893	3	US-08-271-667B-5	Sequence 5, Appli
C 274	30.4	1.3	4870	3	US-09-311-743-7	Sequence 7, Appli	347	29.8	1.2	1893	3	US-08-765-889C-18	Sequence 18, Appli
C 275	30.4	1.3	640681	4	US-09-790-988-1	Sequence 1, Appli	348	29.8	1.2	1893	5	PCT-US95-07855-18	Sequence 18, Appli
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C 279	30.2	1.3	702	4	US-09-252-991A-5549	Sequence 5549, Ap	352	29.8	1.2	2304	1	US-08-271-667B-6	Sequence 6, Appli
C 280	30.2	1.3	868	4	US-09-071-035-71	Sequence 71, Appli	353	29.8	1.2	2304	3	US-08-765-889C-19	Sequence 19, Appli
C 281	30.2	1.3	906	4	US-09-134-000C-2609	Sequence 2609, Ap	354	29.8	1.2	2304	5	PCT-US95-07855-19	Sequence 19, Appli
C 282	30.2	1.3	954	4	US-09-071-035-69	Sequence 69, Appli	355	29.8	1.2	2563	4	US-09-016-434-1076	Sequence 1076, Ap
C 283	30.2	1.3	1014	4	US-09-252-991A-10186	Sequence 10186, A	C 356	29.8	1.2	2563	4	US-09-023-655-894	Sequence 894, App
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C 285	30.2	1.3	1344	4	US-09-252-991A-7741	Sequence 7741, Ap	C 358	29.8	1.2	2601	3	US-08-569-749-3	Sequence 3, Appli
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C 293	30	1.3	434	4	US-09-370-838-68	Sequence 68, Appli	366	29.6	1.2	314	3	US-03-328-111-35	Sequence 35, Appli
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C 298	30	1.3	681	4	US-09-252-991A-14735	Sequence 14735, A	C 371	29.6	1.2	441	4	US-08-914-375C-56	Sequence 56, Appli
C 299	30	1.3	788	2	US-08-883-795A-35	Sequence 35, Appli	372	29.6	1.2	448	4	US-09-621-976-9297	Sequence 9297, Ap
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C 304	30	1.3	1176	5	PCT-US95-15696-1	Sequence 1, Appli	C 377	29.6	1.2	1001	4	US-09-641-638-519	Sequence 519, App
C 305	30	1.3	1219	4	US-09-833-381-840	Sequence 840, App	C 378	29.6	1.2	1001	4	US-09-641-638-520	Sequence 520, App
C 306	30	1.3	1266	4	US-09-252-991A-14898	Sequence 14898, A	C 379	29.6	1.2	1202	4	US-09-494-921-3	Sequence 3, Appli
C 307	30	1.3	1288	1	US-08-440-856A-9	Sequence 9, Appli	380	29.6	1.2	1319	4	US-09-594-506-43	Sequence 12019, A
C 308	30	1.3	1326	4	US-09-625-188-3	Sequence 3, Appli	381	29.6	1.2	1458	4	US-09-252-991A-11964	Sequence 11964, A
C 309	30	1.3	1347	2	US-08-472-172-5	Sequence 5, Appli	C 382	29.6	1.2	1467	4	US-09-328-352-1719	Sequence 352, App
C 310	30	1.3	1788	4	US-09-519-878-3	Sequence 3, Appli	C 383	29.6	1.2	1587	4	US-09-489-039A-5906	Sequence 5906, Ap
C 311	30	1.3	1908	4	US-09-565-501A-109	Sequence 109, App	384	29.6	1.2	1632	4	US-09-328-352-1719	Sequence 352, App
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C 313	30	1.3	1908	4	US-09-874-923-109	Sequence 109, App	386	29.6	1.2	1709	2	US-09-010-398-2	Sequence 2, Appli
C 314	30	1.3	1920	4	US-09-252-991A-8518	Sequence 8518, Ap	387	29.6	1.2	1709	3	US-09-366-260-2	Sequence 2, Appli
C 315	30	1.3	1943	4	US-09-620-312D-396	Sequence 396, App	388	29.6	1.2	1709	3	US-09-153-804-11	Sequence 11, Appli
C 316	30	1.3	1986	4	US-09-252-991A-14474	Sequence 14474, A	389	29.6	1.2	1808	4	US-09-599-360B-38	Sequence 38, Appli
C 317	30	1.3	2033	4	US-09-252-991A-8359	Sequence 8359, Ap	390	29.6	1.2	2091	4	US-09-100-527-1	Sequence 1, Appli
C 318	30	1.3	2201	4	US-09-976-594-485	Sequence 485, App	391	29.6	1.2	2201	4	US-09-449-476-245	Sequence 245, App
C 319	30	1.3	2220	5	PCT-US95-13749-2	Sequence 2, Appli	392	29.6	1.2	2264	4	US-09-833-381-883	Sequence 883, App

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RESULT 2

US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, P.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELE: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ptzapt-F1s
; US-08-232-463-14

[illegible][illegible]

RESULT 3

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US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ptzgmt-Fls
US-08-232-463-14

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Fri Aug 6 10:49:40 2004

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RESULT 4
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063

GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832

TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399

US-09-621-976-2813

Query Match 1.6%; Score 38.8; DB 4; Length 832;
Best Local Similarity 13.6%; Pred. No. 0.11;
Matches 45; Conservative 148; Mismatches 135; Indels 4; Gaps 1;

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RESULT 5
US-09-555-790A-1
; Sequence 1, Application US/09555790A
; Patent No. 6555652
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyoto et al.
; TITLE OF INVENTION: TUMOR ANTIGEN PEPTIDE DERIVATIVES
; FILE REFERENCE: 0020-4716P
; CURRENT APPLICATION NUMBER: US/09/555,790A
; CURRENT FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 2527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(2438)
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (2439)..(2506)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(38)
; US-09-555-790A-1

Query Match 1.6%; Score 37.4; DB 4; Length 2527;
Best Local Similarity 55.9%; Pred. No. 0.68;
Matches 71; Conservative

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Db 1415 GCCCTG 1421

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RESULT 6
US-09-141-000-4/c
; Sequence 4, Application US/09141000
; Patent No. 6054295

GENERAL INFORMATION:
; APPLICANT: Chen, Fang
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NUCLEAR
; TITLE OF INVENTION: RECEPTOR PROTEINS
; FILE REFERENCE: 19999Y
; CURRENT APPLICATION NUMBER: US/09/141,000
; CURRENT FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Human
; US-09-141-000-4

Query Match 1.5%; Score 37; DB 3; Length 458;
Best Local Similarity 9.5%; Pred. No. 0.28;
Matches 31; Conservative 105; Mismatches 190; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2004, 12:54:24 ; Search time 975 Seconds
(without alignments)

10435.317 Million cell updates/sec

Title: US-10-036-150-44

Perfect score: 2395

Sequence: 1 cctggagcggagcgccgcg.....gcaataatgagagaaaaa 2395

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : N Geneseq 23Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2395	100.0	2395	3	AAA96345 cDNA enco
2	2395	100.0	2395	4	Ado2923 Human PRO
3	2395	100.0	2395	4	Adf92127 Human PRO
4	2395	100.0	2395	5	AAc91490 Human PRO
5	2395	100.0	2395	6	ABk33594 cDNA enco
6	2395	100.0	2395	6	ABs74447 Human PRO
7	2395	100.0	2395	6	ABL88217 Human PRO
8	2395	100.0	2395	6	ABL95706 Human ang
9	2395	100.0	2395	7	ACA06159 cDNA enco
10	2395	100.0	2395	7	ACA66899 cDNA enco
11	2395	100.0	2395	7	ACD68651 Novel hum
12	2395	100.0	2395	7	ACA91233 Novel hum
13	2395	100.0	2395	7	ACD81610 Human cDN
14	2395	100.0	2395	7	ACD28828 Human sec
15	2395	100.0	2395	7	ACA60432 Novel hum
16	2395	100.0	2395	7	ACA56879 Human PRO
17	2395	100.0	2395	7	ACA64055 cDNA enco
18	2395	100.0	2395	7	ABX13479 Human DNA
19	2395	100.0	2395	7	ACA06102 cDNA enco
20	2395	100.0	2395	7	ACA91319 cDNA enco
21	2395	100.0	2395	7	ACD45218 Human sec
22	2395	100.0	2395	7	ACA93766 Human cDN
23	2395	100.0	2395	7	ACA67340 cDNA enco

24	2395	100.0	2395	7	ACA68555	Novel hum
25	2395	100.0	2395	7	ACH66313	Novel hum
26	2395	100.0	2395	7	ACD02367	Novel hum
27	2395	100.0	2395	7	ACA89358	Novel hum
28	2395	100.0	2395	7	ACA68995	Novel hum
29	2395	100.0	2395	7	ACA98517	Novel hum
30	2395	100.0	2395	8	ACA63442	Human PRO
31	2395	100.0	2395	8	ACA67725	cDNA enco
32	2395	100.0	2395	8	ADA76569	Novel hum
33	2395	100.0	2395	8	ABT44284	Novel hum
34	2395	100.0	2395	8	ADBI17196	Human PRO
35	2395	100.0	2395	8	ACH03645	Human cDN
36	2395	100.0	2395	8	ACH03645	Human sec
37	2395	100.0	2395	8	ADA20001	Novel hum
38	2395	100.0	2395	8	ADBI17384	Human cDN
39	2395	100.0	2395	8	ADA20173	Novel hum
40	2395	100.0	2395	8	ACB82159	Human PRO
41	2395	100.0	2395	8	ABT44567	Human sec
42	2395	100.0	2395	8	ACD82234	Human PRO
43	2395	100.0	2395	8	ADA00470	Human sec
44	2395	100.0	2395	8	ACD42287	Human cDN
45	2395	100.0	2395	8	ABT43940	Human mem
46	2395	100.0	2395	8	ADB85712	Novel hum
47	2395	100.0	2395	8	ADH83607	Novel hum
48	2395	100.0	2395	8	ADH80713	Novel hum
49	2395	100.0	2395	8	ADB73254	Novel hum
50	2395	100.0	2395	9	ADB84984	Human PRO
51	2395	100.0	2395	9	ADB78090	Novel hum
52	2395	100.0	2395	9	ADH87156	Novel hum
53	2395	100.0	2395	9	ADH84738	Human PRO
54	2395	100.0	2395	9	ADH68391	Human PRO
55	2395	100.0	2395	9	ADH68198	Human PRO
56	2395	100.0	2395	9	ADH83853	Novel hum
57	2395	100.0	2395	9	ADH73008	Novel hum
58	2395	100.0	2395	9	ADH91015	Novel hum
59	2395	100.0	2395	9	ADH59353	Human PRO
60	2395	100.0	2395	9	ADH59228	Human PRO
61	2395	100.0	2395	9	ADC07095	Human PRO
62	2395	100.0	2395	9	ADC17274	cDNA sequ
63	2395	100.0	2395	9	ADC14972	Novel hum
64	2395	100.0	2395	9	ADC36846	Human PRO
65	2395	100.0	2395	9	ADC52467	Novel hum
66	2395	100.0	2395	9	ADC21836	Human PRO
67	2395	100.0	2395	9	ADC29800	Novel hum
68	2395	100.0	2395	9	ADC49867	Novel hum
69	2395	100.0	2395	9	ADC49066	Novel hum
70	2395	100.0	2395	9	ADC45583	Novel hum
71	2395	100.0	2395	9	ADC47444	Novel hum
72	2395	100.0	2395	9	ADC47189	Novel hum
73	2395	100.0	2395	9	ADC78064	Novel hum
74	2395	100.0	2395	9	ADD06299	Novel hum
75	2395	100.0	2395	9	ADD10580	Human sec
76	2395	100.0	2395	9	ADC77818	Novel hum
77	2395	100.0	2395	9	ADD11540	Human sec
78	2395	100.0	2395	9	ADD50781	Novel hum
79	2395	100.0	2395	9	ADD15377	Novel hum
80	2395	100.0	2395	9	ADD51027	Novel hum
81	2395	100.0	2395	9	ADD37333	Human sec
82	2395	100.0	2395	9	ADD36143	Novel hum
83	2395	100.0	2395	9	ADD50508	Human PRO
84	2395	100.0	2395	9	ADD50262	Human PRO
85	2395	100.0	2395	9	ADD51273	Novel hum
86	2395	100.0	2395	10	ADC48820	Novel hum
87	2395	100.0	2395	10	ADC52277	Novel hum
88	2395	100.0	2395	10	ADE20991	Novel hum
89	2395	100.0	2395	10	ADE05835	Human PRO
90	2395	100.0	2395	10	ADD75064	Human PRO
91	2395	100.0	2395	10	ADD75810	Novel hum
92	2395	100.0	2395	10	ADD85042	Novel hum
93	2395	100.0	2395	10	ADD86868	Novel hum
94	2395	100.0	2395	10	ADE20745	Novel hum
95	2395	100.0	2395	10	ADE39042	Novel hum
96	2395	100.0	2395	10	ADE05589	Human PRO

97	2395	100.0	2395	10	ADD73574	Add73574 Human PRO	170	101.8	4.3	3671	7	ACA73517	ACA73517 Human sec
98	2395	100.0	2395	10	ADD78414	Add78414 Novel hum	171	101.8	4.3	3671	7	ACA05832	Human sec
99	2395	100.0	2395	10	ADE41541	Ade41541 Human sec	172	101.8	4.3	3671	7	ACA66666	CDNA enco
100	2395	100.0	2395	10	ADE21237	Ade21237 Novel hum	173	101.8	4.3	3671	7	ACF19627	Human sec
101	2395	100.0	2395	10	ADD77352	Add77352 Novel hum	174	101.8	4.3	3671	7	ACF19627	Human sec
102	2395	100.0	2395	10	ADE20499	Ade20499 Novel hum	175	101.8	4.3	3671	7	ACD21915	Human sec
103	2395	100.0	2395	10	ADD75564	Add75564 Human PRO	176	101.8	4.3	3671	7	ACF13080	Human sec
104	2395	100.0	2395	10	ADD74080	Add74080 Human PRO	177	101.8	4.3	3671	7	ACD25183	Human sec
105	2395	100.0	2395	10	ADD74326	Add74326 Human PRO	178	101.8	4.3	3671	7	ACF00232	Human sec
106	2395	100.0	2395	10	ADD76056	Add76056 Novel hum	179	101.8	4.3	3671	7	ACA72289	Novel hum
107	2395	100.0	2395	10	ADD85548	Add85548 Novel hum	180	101.8	4.3	3671	7	ACD04813	Novel hum
108	2395	100.0	2395	10	ADE05097	Ade05097 Human PRO	181	101.8	4.3	3671	7	ACD18274	Human sec
109	2395	100.0	2395	10	ADD75310	Add75310 Human PRO	182	101.8	4.3	3671	7	ACD08281	Human sec
110	2395	100.0	2395	10	ADD76854	Add76854 Novel hum	183	101.8	4.3	3671	7	ACA88715	Human sec
111	2395	100.0	2395	10	ADD86622	Add86622 Novel hum	184	101.8	4.3	3671	7	ACA70157	Human sec
112	2395	100.0	2395	10	ADD78090	Add78090 Novel hum	185	101.8	4.3	3671	7	ACD12379	Novel hum
113	2395	100.0	2395	10	ADD77598	Add77598 Novel hum	186	101.8	4.3	3671	7	ACC74294	Human sec
114	2395	100.0	2395	10	ADD77844	Add77844 Novel hum	187	101.8	4.3	3671	7	ACD15922	Human sec
115	2395	100.0	2395	10	ADD85302	Add85302 Novel hum	188	101.8	4.3	3671	7	ACD25490	Novel hum
116	2395	100.0	2395	10	ADD73834	Add73834 Human PRO	189	101.8	4.3	3671	7	ACD88254	Human sec
117	2395	100.0	2395	10	ADD74572	Add74572 Human PRO	190	101.8	4.3	3671	7	ACD17967	Human sec
118	2395	100.0	2395	10	ADD77100	Add77100 Novel hum	191	101.8	4.3	3671	7	ACD21608	Human sec
119	2395	100.0	2395	10	ADD85794	Add85794 Novel hum	192	101.8	4.3	3671	7	ACD18675	Human sec
120	2395	100.0	2395	10	ADE05343	Ade05343 Human PRO	193	101.8	4.3	3671	7	ABX98285	Human cDN
121	2395	100.0	2395	10	ADD74818	Add74818 Human PRO	194	101.8	4.3	3671	7	ACD14036	Human PRO
122	1521.2	63.5	3197	4	AAK94266	AAK94266 Human ful	195	101.8	4.3	3671	7	ACD09816	Human sec
123	1417.6	59.2	2952	9	ADE07088	Ade07088 Novel cod	196	101.8	4.3	3671	7	ACC88561	Human sec
124	1266.6	52.9	3019	9	AAK94714	AAK94714 Human ful	197	101.8	4.3	3671	7	ACD21301	Human cDN
125	1023.8	42.7	3310	9	AD872573	Ade72573 Human end	198	101.8	4.3	3671	7	ABX75673	Human PRO
126	992.2	41.4	2755	6	ABN59875	ABN59875 Novel hum	199	101.8	4.3	3671	7	ABX97876	Human PRO
127	824	34.4	857	4	AAK93328	AAK93328 Human cDN	200	101.8	4.3	3671	7	ACA97352	Novel hum
128	808	33.7	816	9	ADE08866	Ade08866 Novel DNA	201	101.8	4.3	3671	7	ACA57815	Human PRO
129	731.6	30.5	818	4	AAK93603	AAK93603 Human cDN	202	101.8	4.3	3671	7	ACD14343	Human PRO
130	731.6	30.5	818	4	AAK91771	AAK91771 Human cDN	203	101.8	4.3	3671	7	ACC88868	Human sec
131	510.4	21.3	566	4	AAK93941	AAK93941 Human cDN	204	101.8	4.3	3671	7	ACD07065	Human sec
132	510.4	21.3	566	4	AAK91872	AAK91872 Human cDN	205	101.8	4.3	3671	7	ACD07065	Human sec
133	455.6	19.0	500	8	ACH34160	Ach34160 Human end	206	101.8	4.3	3671	7	ACA67516	Human PRO
134	411.4	17.2	451	5	ABH412238	ABH412238 Human ner	207	101.8	4.3	3671	7	ACC81571	Human sec
135	277.4	11.6	801	4	AAH05366	AAH05366 Human cDN	208	101.8	4.3	3671	7	ACC89175	Human sec
136	277.4	11.6	1966	4	AAH14070	AAH14070 Human cDN	209	101.8	4.3	3671	7	ACC86531	Human sec
137	213.8	8.9	848	9	ADE72574	Ade72574 Human end	210	101.8	4.3	3671	7	ACC89789	Human sec
138	153	6.4	553	6	ABQ45840	Abq45840 Oligonuc	211	101.8	4.3	3671	7	ACA92596	Human sec
139	146.2	6.1	553	6	ABQ45841	Abq45841 Oligonuc	212	101.8	4.3	3671	7	ACA92596	Human sec
140	146.2	6.1	553	6	ABQ45839	Abq45839 Oligonuc	213	101.8	4.3	3671	7	ACA89114	Human sec
141	146.2	6.1	553	6	ABQ45838	Abq45838 Oligonuc	214	101.8	4.3	3671	7	ACA69850	Human sec
142	101.8	4.3	1818	7	AAH05979	AAH05979 Human sec	215	101.8	4.3	3671	7	ACA96993	Novel hum
143	101.8	4.3	2559	7	AAH55964	AAH55964 Human sec	216	101.8	4.3	3671	7	ACA90989	Novel hum
144	101.8	4.3	2717	8	AAH55978	AAH55978 Human sec	217	101.8	4.3	3671	7	ACA70771	Human sec
145	101.8	4.3	2717	8	AAH55955	AAH55955 Human sec	218	101.8	4.3	3671	7	ACA95281	Novel hum
146	101.8	4.3	2744	3	AAH98909	AAH98909 Human EST	219	101.8	4.3	3671	7	ACC86224	Human sec
147	101.8	4.3	3671	3	AAAF37051	AAAF37051 Human PRO	220	101.8	4.3	3671	7	ACC90096	Human sec
148	101.8	4.3	3671	4	AAAF54273	AAAF54273 DNA enco	221	101.8	4.3	3671	7	ACD12704	Human sec
149	101.8	4.3	3671	4	AAAF46057	AAAF46057 Human DNA	222	101.8	4.3	3671	7	ACF19934	Human sec
150	101.8	4.3	3671	4	ABX78660	ABX78660 Human PRO	223	101.8	4.3	3671	7	ABX76878	Human PRO
151	101.8	4.3	3671	7	ACA75632	ACA75632 Novel hum	224	101.8	4.3	3671	7	ACA73210	Novel hum
152	101.8	4.3	3671	7	ACA71112	ACA71112 Human sec	225	101.8	4.3	3671	7	ACA68753	Novel hum
153	101.8	4.3	3671	7	ACC87640	ACC87640 Human sec	226	101.8	4.3	3671	7	ACA74597	CDNA enco
154	101.8	4.3	3671	7	ACC87026	ACC87026 Human sec	227	101.8	4.3	3671	7	ACA70464	Human sec
155	101.8	4.3	3671	7	ACD04199	ACD04199 Human sec	228	101.8	4.3	3671	7	ABX98787	Novel hum
156	101.8	4.3	3671	7	ACA69530	ACA69530 cDNA enco	229	101.8	4.3	3671	7	ACD14650	Human PRO
157	101.8	4.3	3671	7	ACA90375	ACA90375 Novel hum	230	101.8	4.3	3671	7	ABX98787	Novel hum
158	101.8	4.3	3671	7	ACC89482	ACC89482 Human sec	231	101.8	4.3	3671	7	ACC81264	Human sec
159	101.8	4.3	3671	7	ACA98273	ACA98273 Novel hum	232	101.8	4.3	3671	7	ACA95588	Novel hum
160	101.8	4.3	3671	7	ACA93915	ACA93915 Human sec	233	101.8	4.3	3671	7	ACD04506	Human sec
161	101.8	4.3	3671	7	ACD08895	ACD08895 Human sec	234	101.8	4.3	3671	7	ACC87947	Human sec
162	101.8	4.3	3671	7	ACD15308	ACD15308 Human sec	235	101.8	4.3	3671	7	ACF12609	Human PRO
163	101.8	4.3	3671	7	ACC96815	ACC96815 Human sec	236	101.8	4.3	3671	7	ACA65098	Human PRO
164	101.8	4.3	3671	7	ACF15536	ACF15536 Human sec	237	101.8	4.3	3671	7	ACA73824	Human sec
165	101.8	4.3	3671	7	ACA72903	ACA72903 Human PRO	238	101.8	4.3	3671	7	ACA74236	Novel hum
166	101.8	4.3	3671	7	ACD03075	ACD03075 Novel hum	239	101.8	4.3	3671	7	ACA96631	Human PRO
167	101.8	4.3	3671	7	ACA92082	ACA92082 Novel hum	240	101.8	4.3	3671	7	ACD10737	CDNA enco
168	101.8	4.3	3671	7	ACA89507	ACA89507 cDNA enco	241	101.8	4.3	3671	7	ACC91433	Human sec
169	101.8	4.3	3671	7			242	101.8	4.3	3671	7		

243	101.8	4.3	3671	7	ACD02768	Acc87333	CDNA	enco	316	101.8	4.3	3671	8	ACD09509	Acc87333	Human	sec
244	101.8	4.3	3671	7	ACC87333	Acc87333	Human	sec	317	101.8	4.3	3671	8	ACD08588	Acc87333	Human	sec
245	101.8	4.3	3671	7	ACC85917	Acc85917	Human	sec	318	101.8	4.3	3671	8	ACF12302	Acc85917	Human	sec
246	101.8	4.3	3671	7	ACA85405	ACA85405	Human	PRO	319	101.8	4.3	3671	8	ACC94810	ACA85405	Human	sec
247	101.8	4.3	3671	7	ACA94222	ACA94222	Human	sec	320	101.8	4.3	3671	8	ACC22529	ACA94222	Human	sec
248	101.8	4.3	3671	7	ACA97966	ACA97966	Human	PRO	321	101.8	4.3	3671	8	ACF15229	ACA97966	Human	sec
249	101.8	4.3	3671	7	ACA91468	ACA91468	Novel	hum	322	101.8	4.3	3671	8	ACC97324	ACA91468	Human	sec
250	101.8	4.3	3671	7	ACA90682	ACA90682	Novel	hum	323	101.8	4.3	3671	8	ACC92354	ACA90682	Human	sec
251	101.8	4.3	3671	7	ACD16229	ACD16229	Human	sec	324	101.8	4.3	3671	8	ACF14001	ACD16229	Human	sec
252	101.8	4.3	3671	7	ACD17390	ACD17390	Human	sec	325	101.8	4.3	3671	8	ACF14308	ACD17390	Human	sec
253	101.8	4.3	3671	7	ACC92047	ACC92047	Human	sec	326	101.8	4.3	3671	8	ACF09539	ACC92047	Human	sec
254	101.8	4.3	3671	7	ACA74904	ACA74904	CDNA	enco	327	101.8	4.3	3671	8	ACD68310	ACA74904	Novel	hum
255	101.8	4.3	3671	7	ACA91775	ACA91775	Human	PRO	328	101.8	4.3	3671	8	ACD45830	ACA91775	Human	sec
256	101.8	4.3	3671	7	ACA71419	ACA71419	Human	sec	329	101.8	4.3	3671	8	ACD47979	ACA71419	Human	sec
257	101.8	4.3	3671	7	ACC90819	ACC90819	Human	sec	330	101.8	4.3	3671	8	ACD67710	ACC90819	CDNA	enco
258	101.8	4.3	3671	7	ACA55829	ACA55829	Human	sec	331	101.8	4.3	3671	8	ACF25518	ACA55829	Human	sec
259	101.8	4.3	3671	7	ACA94974	ACA94974	CDNA	enco	332	101.8	4.3	3671	8	ACF29202	ACA94974	Human	sec
260	101.8	4.3	3671	7	ACD16536	ACD16536	Human	sec	333	101.8	4.3	3671	8	ACD84980	ACD16536	Human	sec
261	101.8	4.3	3671	7	ACD15615	ACD15615	Human	sec	334	101.8	4.3	3671	8	ACD84059	ACD15615	Human	PRO
262	101.8	4.3	3671	7	ABX16718	ABX16718	Human	CDN	335	101.8	4.3	3671	8	ACD88050	ABX16718	Human	sec
263	101.8	4.3	3671	8	ACA97659	ACA97659	Human	PRO	336	101.8	4.3	3671	8	ACF30737	ACA97659	Human	sec
264	101.8	4.3	3671	8	ACA99108	ACA99108	Novel	hum	337	101.8	4.3	3671	8	ACF32340	ACA99108	Human	sec
265	101.8	4.3	3671	8	ACC91740	ACC91740	Human	sec	338	101.8	4.3	3671	8	ACH12000	ACC91740	CDNA	enco
266	101.8	4.3	3671	8	ACD11151	ACD11151	Novel	hum	339	101.8	4.3	3671	8	ACH12307	ACD11151	CDNA	enco
267	101.8	4.3	3671	8	ACD15001	ACD15001	Human	sec	340	101.8	4.3	3671	8	ACD40699	ACD15001	Human	sec
268	101.8	4.3	3671	8	ACC95894	ACC95894	Human	sec	341	101.8	4.3	3671	8	ACF18171	ACC95894	Human	sec
269	101.8	4.3	3671	8	ACF16457	ACF16457	Human	sec	342	101.8	4.3	3671	8	ACF08618	ACF16457	Human	sec
270	101.8	4.3	3671	8	ACF02575	ACF02575	Human	sec	343	101.8	4.3	3671	8	ACF31419	ACF02575	Human	sec
271	101.8	4.3	3671	8	ACF02882	ACF02882	Human	sec	344	101.8	4.3	3671	8	ACF52259	ACF02882	Human	sec
272	101.8	4.3	3671	8	ACF21469	ACF21469	Human	sec	345	101.8	4.3	3671	8	ACD50128	ACF21469	Human	sec
273	101.8	4.3	3671	8	ACF10153	ACF10153	Human	sec	346	101.8	4.3	3671	8	ACF38831	ACF10153	Human	sec
274	101.8	4.3	3671	8	ACF78046	ACF78046	Human	sec	347	101.8	4.3	3671	8	ACF26746	ACF78046	Human	sec
275	101.8	4.3	3671	8	ACD46751	ACD46751	Human	sec	348	101.8	4.3	3671	8	ACF24846	ACD46751	Human	sec
276	101.8	4.3	3671	8	ACD49514	ACD49514	Human	sec	349	101.8	4.3	3671	8	ACF46426	ACD49514	Human	sec
277	101.8	4.3	3671	8	ACD88971	ACD88971	Human	sec	350	101.8	4.3	3671	8	ACF27974	ACD88971	Human	sec
278	101.8	4.3	3671	8	ACD84366	ACD84366	Human	PRO	351	101.8	4.3	3671	8	ACD89278	ACD84366	Human	sec
279	101.8	4.3	3671	8	ACD99140	ACD99140	CDNA	enco	352	101.8	4.3	3671	8	ACF63850	ACD99140	Human	sec
280	101.8	4.3	3671	8	ADA78017	ADA78017	Human	sec	353	101.8	4.3	3671	8	ACF60490	ADA78017	Human	sec
281	101.8	4.3	3671	8	ACF48882	ACF48882	Human	sec	354	101.8	4.3	3671	8	ACH12614	ACF48882	CDNA	enco
282	101.8	4.3	3671	8	ACF48882	ACF48882	Human	sec	355	101.8	4.3	3671	8	ACH10037	ACF48882	Human	sec
283	101.8	4.3	3671	8	ACF48882	ACF48882	Human	sec	356	101.8	4.3	3671	8	ACD03892	ACF48882	Human	sec
284	101.8	4.3	3671	8	ACF11995	ACF11995	Human	sec	357	101.8	4.3	3671	8	ACD10430	ACF11995	Human	sec
285	101.8	4.3	3671	8	ACF15843	ACF15843	Human	sec	358	101.8	4.3	3671	8	ACF42457	ACF15843	Human	sec
286	101.8	4.3	3671	8	ACF15843	ACF15843	Human	sec	359	101.8	4.3	3671	8	ACF18478	ACF15843	Human	sec
287	101.8	4.3	3671	8	ACF16150	ACF16150	Human	sec	360	101.8	4.3	3671	8	ACF02268	ACF16150	Human	sec
288	101.8	4.3	3671	8	ACD31977	ACD31977	Human	sec	361	101.8	4.3	3671	8	ACF21776	ACD31977	Human	sec
289	101.8	4.3	3671	8	ACF18785	ACF18785	Human	sec	362	101.8	4.3	3671	8	ACF10460	ACF18785	Human	sec
290	101.8	4.3	3671	8	ACF09232	ACF09232	Human	sec	363	101.8	4.3	3671	8	ACF33912	ACF09232	Human	sec
291	101.8	4.3	3671	8	ACF78353	ACF78353	Human	sec	364	101.8	4.3	3671	8	ACF44874	ACF78353	Human	sec
292	101.8	4.3	3671	8	ACF51952	ACF51952	Human	sec	365	101.8	4.3	3671	8	ACD90506	ACF51952	Human	sec
293	101.8	4.3	3671	8	ACF26439	ACF26439	Human	sec	366	101.8	4.3	3671	8	ACD91119	ACF26439	Human	sec
294	101.8	4.3	3671	8	ACF24232	ACF24232	Human	sec	367	101.8	4.3	3671	8	ACF30430	ACF24232	Human	sec
295	101.8	4.3	3671	8	ACF63543	ACF63543	Human	sec	368	101.8	4.3	3671	8	ACD87129	ACF63543	Human	sec
296	101.8	4.3	3671	8	ACH07888	ACH07888	Human	sec	369	101.8	4.3	3671	8	ACF60183	ACH07888	Human	sec
297	101.8	4.3	3671	8	ACF13694	ACF13694	Human	sec	370	101.8	4.3	3671	8	ACF46733	ACF13694	Human	sec
298	101.8	4.3	3671	8	ACD41620	ACD41620	Human	sec	371	101.8	4.3	3671	8	ACF75590	ACD41620	Human	sec
299	101.8	4.3	3671	8	ACF32033	ACF32033	Human	sec	372	101.8	4.3	3671	8	ACF46733	ACF32033	Human	sec
300	101.8	4.3	3671	8	ACF23311	ACF23311	Human	sec	373	101.8	4.3	3671	8	ACF75590	ACF23311	Human	sec
301	101.8	4.3	3671	8	ACF40001	ACF40001	Human	sec	374	101.8	4.3	3671	8	ACF17250	ACF40001	Human	sec
302	101.8	4.3	3671	8	ACD45523	ACD45523	Human	sec	375	101.8	4.3	3671	8	ACF23004	ACD45523	Human	sec
303	101.8	4.3	3671	8	ACF53180	ACF53180	Human	sec	376	101.8	4.3	3671	8	ACF08004	ACF53180	Human	sec
304	101.8	4.3	3671	8	ACF27360	ACF27360	Human	sec	377	101.8	4.3	3671	8	ACF40615	ACF27360	Human	sec
305	101.8	4.3	3671	8	ACF45198	ACF45198	Human	sec	378	101.8	4.3	3671	8	ACF53794	ACF45198	Human	sec
306	101.8	4.3	3671	8	ACF29816	ACF29816	Human	sec	379	101.8	4.3	3671	8	ACF47058	ACF29816	Human	sec
307	101.8	4.3	3671	8	ACD84673	ACD84673	Human	sec	380	101.8	4.3	3671	8	ACF47961	ACD84673	Human	sec
308	101.8	4.3	3671	8	ACD89892	ACD89892	Human	sec	381	101.8	4.3	3671	8	ACF47347	ACD89892	Human	sec
309	101.8	4.3	3671	8	ACF98833	ACF98833	CDNA	enco	382	101.8	4.3	3671	8	ACF46119	ACF98833	Human	sec
310	101.8	4.3	3671	8	ACF77125	ACF77125	Human	sec	383	101.8	4.3	3671	8	ACD86208	ACF77125	Human	sec
311	101.8	4.3	3671	8	ACF6818	ACF6818	Human	sec	384	101.8	4.3	3671	8	ACF52566	ACF6818	Human	sec
312	101.8	4.3	3671	8	ACF49803	ACF49803	Human	sec	385	101.8	4.3	3671	8	ACF52873	ACF49803	Human	sec
313	101.8	4.3	3671	8	ACF50110	ACF50110	Human	sec	386	101.8	4.3	3671	8	ACF64866	ACF50110	Human	sec
314	101.8	4.3	3671	8	ACF50110	ACF50110	Human	sec	387	101.8	4.3	3671	8	ACF76511	ACF50110	Human	sec
315	101.8	4.3	3671	8	ACF50110	ACF50110	Human	sec	388	101.8	4.3	3671	8	ACF76511	ACF50110	Human	sec

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Fri Aug 6 10:49:39 2004

389	101.8	4.3	3671	8	ACF61411	Human sec
390	101.8	4.3	3671	8	ACF61718	Human sec
391	101.8	4.3	3671	8	ACD30749	Human sec
392	101.8	4.3	3671	8	ACD31670	Human sec
393	101.8	4.3	3671	8	ACD32591	Human sec
394	101.8	4.3	3671	8	ACF17557	Human sec
395	101.8	4.3	3671	8	ACF07390	Human sec
396	101.8	4.3	3671	8	ACF20548	Human sec
397	101.8	4.3	3671	8	ACF20855	Human sec
398	101.8	4.3	3671	8	ACF21162	Human sec
399	101.8	4.3	3671	8	ACD47672	Human sec
400	101.8	4.3	3671	8	ACF47654	Human sec
401	101.8	4.3	3671	8	ACF53487	Human sec
402	101.8	4.3	3671	8	ACD86822	Human sec
403	101.8	4.3	3671	8	ACH05070	CDNA enco
404	101.8	4.3	3671	8	ACF44567	Human sec
405	101.8	4.3	3671	8	ADA81536	Human sec
406	101.8	4.3	3671	8	ACD22222	Human sec
407	101.8	4.3	3671	8	ACD24569	Human sec
408	101.8	4.3	3671	8	ACD39772	CDNA enco
409	101.8	4.3	3671	8	ACD40079	CDNA enco
410	101.8	4.3	3671	8	ACF13387	Human sec
411	101.8	4.3	3671	8	ACF03189	Human sec
412	101.8	4.3	3671	8	ACF78660	Human sec
413	101.8	4.3	3671	8	ACF11381	Human sec
414	101.8	4.3	3671	8	ACF50724	Human sec
415	101.8	4.3	3671	8	ACD46444	Human sec
416	101.8	4.3	3671	8	ACD27667	Human sec
417	101.8	4.3	3671	8	ACF24539	Human sec
418	101.8	4.3	3671	8	ACD85594	Human sec
419	101.8	4.3	3671	8	ACD90199	Human sec
420	101.8	4.3	3671	8	ACD83752	Human sec
421	101.8	4.3	3671	8	ACF49189	Human sec
422	101.8	4.3	3671	8	ACH07274	Human sec
423	101.8	4.3	3671	8	ACH07581	Human sec
424	101.8	4.3	3671	8	ACH07581	Human sec
425	101.8	4.3	3671	8	ACH08195	Human sec
426	101.8	4.3	3671	8	ACH11386	CDNA enco
427	101.8	4.3	3671	8	ACH11693	CDNA enco
428	101.8	4.3	3671	8	ACH10344	Human sec
429	101.8	4.3	3671	8	ACH10347	Human sec
430	101.8	4.3	3671	8	ACH10347	Human sec
431	101.8	4.3	3671	8	ACH10347	Human sec
432	101.8	4.3	3671	8	ACH10347	Human sec
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436	101.8	4.3	3671	8	ACH10347	Human sec
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459	101.8	4.3	3671	8	ACH10347	Human sec
460	101.8	4.3	3671	8	ACH10347	Human sec
461	101.8	4.3	3671	8	ACH10347	Human sec

ALIGNMENTS

RESULT 1

AAA96345

ID AAA96345 standard; cDNA; 2395 BP.

XX AAA96345;

AC AAA96345;

DT 08-FEB-2001 (first entry)

XX cDNA encoding a novel polypeptide designated PRO4405.

DE Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
 XX PRO1899; PRO1890; PRO1887; PRO4353; PRO4405; PRO4356;
 KW PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO5990; PRO6030;
 KW PRO4424; PRO4422; PRO4430; tumour; obesity; diabetes;
 KW insulinemia; kidney disorder; Bergers disease; nephropathy;
 KW Schonelein-Henoch purpura; celiac disease; dermatitis herpetiformis;
 KW Crohns disease; ss.

XX Homo sapiens.

OS Key Location/Qualifiers

FT CDS 79..1011

FT sig_peptide /*tag= a

FT 79..180

XX /*tag= b

PN WO200056889-A2.

XX 28-SEP-2000.

PD

XX PF 01-MAR-2000; 2000WQ-US005601.
XX PR 23-MAR-1999; 99US-0125774P.
XX PR 24-MAR-1999; 99US-0125778P.
XX PR 24-MAR-1999; 99US-0125826P.
XX PR 31-MAR-1999; 99US-0127035P.
XX PR 05-APR-1999; 99US-0127706P.
XX PR 21-APR-1999; 99US-0130359P.
XX PR 27-APR-1999; 99US-0131270P.
XX PR 27-APR-1999; 99US-0131272P.
XX PR 27-APR-1999; 99US-0131291P.
XX PR 04-MAY-1999; 99US-0132371P.
XX PR 04-MAY-1999; 99US-0132379P.
XX PR 04-MAY-1999; 99US-0132383P.
XX PR 25-MAY-1999; 99US-0135750P.
XX PR 08-JUN-1999; 99US-0138166P.
XX PR 20-JUL-1999; 99US-0144791P.
XX PR 03-AUG-1999; 99US-0146970P.
XX PR 09-DEC-1999; 99US-0170262P.
XX PA (GETH) GENENTECH INC.
XX PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
XX PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX DR P-PSDB; AAB18918.
XX DR WPI; 2000-628263/60.
XX PT Novel secreted and transmembrane polypeptides useful for diagnosing tumor
XX PT in a mammal, for identifying agonists and antagonists of the polypeptide
XX PT and for therapeutic use.
XX PS Claim 2; Fig 19; 222pp; English.
XX CC The present sequence encodes a secreted or transmembrane polypeptide. The
XX CC specification describes polypeptides designated PRO1484, PRO4334,
XX CC PRO1122, PRO1989, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
XX CC PRO4356, PRO4352, PRO4380, PRO4354, PRO5737, PRO4425, PRO5990,
XX CC PRO6030, PRO4424, PRO4420, and PRO4499. PRO1889 polypeptide is
XX CC useful for diagnosing tumour in a mammal. The polypeptides, their
XX CC agonists and antagonists are useful treating a condition associated with
XX CC expression or activity of the polypeptide. Conditions treated include
XX CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are
XX CC capable of inducing proliferation of mammalian kidney mesangial cells and
XX CC are therefore useful for treating kidney disorders associated with
XX CC decreased mesangial cell function such as Berger's disease or other
XX CC nephropathies associated with Schönlein-Henoch purpura, celiac disease,
XX CC dermatitis herpetiformis or Crohn's disease. The nucleic acids may be used
XX CC to generate transgenic animals for use in development and screening of
XX CC therapeutically useful reagents and also for chromosome identification
XX CC and tissue typing
XX SQ Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;
Query Match 100.0%; Score 2395; DB 3; Length 2395;
Best Local Similarity 100.0%; Pred. No 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB |||||
QY 1 CCTGGAGCCGGAGCGCGGTGACGAGCGGCTCCAGGTCGGGTCCGGTCCGATC 60
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QY 61 CAGCCTAGCTGTCACAGTCGGCTCGGCTCCGGATTCGCTACCTGTTGCGTAGCG 120
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QY 181 TCTGCGAGCGGAAACACGAGCGGAGCCGCCAGCGCCGACCTCGGCTGAGCGCAGT 240
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181 TCTGCGAGCGGAAACACGAGCGGAGCCGCCAGCGCCGAAACCCCTCGGCTGGAGCCAGT 240
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 1861 GGAAGAAGAGACAATCGGCTCGACACTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
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 2281 CTGCACTCTGCGGCT 2340
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 2341 CTGCAACAGTATGATGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2395
 2341 CTGCAACAGTATGATGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2395

RESULT 2
 AAD02923
 ID AAD02923 standard; cDNA; 2395 BP.
 XX
 AC AAD02923;
 DT
 XX 31-MAY-2001 (first entry)
 XX Human PRO4405 cDNA (DNA84920-2614).
 XX Human; PRO4405; antiinflammatory; dermatological; immunosuppressive;
 XX antirheumatic; antiarthritic; osteopathic; antianemic; haemostatic;
 KW antithyroid; antidiabetic; antiviral; antipsoriatic; antiallergic;
 KW antiaesthetic; inhibitor; therapy; systemic lupus erythematosus;
 KW spondyloarthropathy; systemic sclerosis; systemic vasculitis;
 KW sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome;
 KW autoimmune thrombocytopenia; immune-mediated renal disease; hepatitis;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome; Whipple's disease;
 KW hepatobiliary disease; primary biliary cirrhosis; sclerosing cholangitis;
 KW inflammatory bowel disease; gluten-sensitive enteropathy; skin disease;
 KW allergic rhinitis; atopic dermatitis; food hypersensitivity; urticaria;
 KW eosinophilic pneumonia; hypersensitivity pneumonitis; graft rejection;
 KW idiopathic pulmonary fibrosis; graft-versus-host-disease; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
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 FT sig_peptide 79..180
 /tag= b
 FT mat_peptide 181..1008
 /tag= c
 /product= "Mature human PRO4405 protein"
 FT
 XX WO200116319-A2.
 XX 08-MAR-2001.
 XX 23-AUG-2000; 2000WO-US023522.
 XX 31-AUG-1999; 99US-0151733P.
 XX 01-SEP-1999; 99WO-US020111.
 XX 16-DEC-1999; 99WO-US030095.
 XX 18-FEB-2000; 2000WO-US004342.
 XX 01-MAR-2000; 2000WO-US005601.
 XX 30-MAR-2000; 2000WO-US008439.
 XX 17-MAY-2000; 2000WO-US013705.
 XX 22-MAY-2000; 2000WO-US014042.
 XX 30-MAY-2000; 2000WO-US014941.
 XX 05-JUN-2000; 2000US-0209832P.
 XX (GETH) GENENTECH INC.
 XX Goddard A, Godowski PU, Gurney AL, Hillan KJ, Tumas D;
 XX Watanabe CK, Wood WI;
 XX WPI; 2001-226690/23.
 XX P-FSDB; AAY72877.
 XX
 XX New PRO polypeptides for treating immune related and inflammatory
 XX diseases such as rheumatoid arthritis, systemic vasculitis, asthma,
 XX autoimmune hemolytic anemia, and diabetes mellitus.
 XX
 XX Claim 2; Fig 7; 118pp; English.
 XX
 XX The present sequence is a cDNA (DNA84920-2614 clone) encoding PRO4405
 XX protein. PRO protein, its agonist or antagonist or its antibody which are
 XX capable of enhancing or inhibiting the proliferation of T-lymphocytes or
 XX of increasing the infiltration of inflammatory cells into a tissue are
 XX useful in the diagnosis and treatment of immune-related diseases in

mammals. The PRO protein is useful for treating systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthritis, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic inflammatory demyelinating polyneuropathy, hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, autoimmune or immune-mediated skin diseases such as bullous skin disease, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, transplantation associated diseases such as graft rejection or graft-versus-host-disease

Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;

Query Match 100.0%; Score 2395; DB 4; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAGCGGAGCGCGGTGACGAGCGGAGGCTCCAGTGGGGTGGTTCGCGATC 60
DB 1 CTTGAGCGGAGCGCGGTGACGAGCGGAGGCTCCAGTGGGGTGGTTCGCGATC 60

QY 61 CAGCTAGCGGTGTCACAGTGGGTGGCTCCGGGACTTGGCTACCTGTTGGCTAGG 120
DB 61 CAGCTAGCGGTGTCACAGTGGGTGGCTCCGGGACTTGGCTACCTGTTGGCTAGG 120

QY 121 ATCAGGTGCTAGGATCGCGTCTTCTTGGGGATCTTCCGGCTCCGGTTCGTTCC 180
DB 121 ATCAGGTGCTAGGATCGCGTCTTCTTGGGGATCTTCCGGCTCCGGTTCGTTCC 180

QY 181 TCTGCGAGCGGAGACGAGCGGAGCGCCCGAGCCCGAACCTCGGCTGGAGCCAGT 240
DB 181 TCTGCGAGCGGAGACGAGCGGAGCGCCCGAGCCCGAACCTCGGCTGGAGCCAGT 240

QY 241 TCTAACTGGACCGCTCCACCGCTCTCTCTAGTAAAGTGTATGTTCTGATAGAT 300
DB 241 TCTAACTGGACCGCTCCACCGCTCTCTCTAGTAAAGTGTATGTTCTGATAGAT 300

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DB 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGCTGTGAATTTATGCCCTACACACT 360

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DB 421 ACTATGCTCGAATCAAGGCAATGATGACGGGAGCCCTTCTGGCTTGTGAGCTCATC 480

QY 481 AGGAACCTCAATTCCTGCACTGCTGGAAGACAGTGTGTAAGACAAAGAGCAGCT 540
DB 481 AGGAACCTCAATTCCTGCACTGCTGGAAGACAGTGTGTAAGACAAAGAGCAGCT 540

QY 541 GGAAAGAGATAGTCTTTTATGGAGATGAACCTGGGTAAATTTATCCCAAGCATTTT 600
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QY 661 GTACGAGGCAATTTGGATAAAGTATTAAGAGAGGAGATTGGGACATATTAATCCTCC 720
DB 661 GTACGAGGCAATTTGGATAAAGTATTAAGAGAGGAGATTGGGACATATTAATCCTCC 720

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QY 781 AAGCTGAGCGAGATGGACAGCGTGTGTATGAAGATCCACACCTCACTGTCAGTCGAGGAG 840
DB 781 AAGCTGAGCGAGATGGACAGCGTGTGTATGAAGATCCACACCTCACTGTCAGTCGAGGAG 840

QY 841 AGAGAGAGCGCTTTACCCAAATTTGCTGTTCTTTTGTGGTACCATGGCATGCTGAAACA 900
DB 841 AGAGAGAGCGCTTTACCCAAATTTGCTGTTCTTTTGTGGTACCATGGCATGCTGAAACA 900

QY 901 GGAAGTCACGGGCTCTCTCCACCGAGGAGTGAATACACCTCTGATTTTAAATCAGTTCT 960
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QY 961 GGGTTTGAAGAAACCCCGGTGATATCCGACATCCAAAGCAGTCCATAGACGATGTG 1020
DB 961 GGGTTTGAAGAAACCCCGGTGATATCCGACATCCAAAGCAGTCCATAGACGATGTG 1020

QY 1021 GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGAGCCTC 1080
DB 1021 GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGAGCCTC 1080

QY 1081 CTATTTCCAGTTTGTGGAAGAGAACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140
DB 1081 CTATTTCCAGTTTGTGGAAGAGAACCAATGAGAGAGCAGTTGAGATTTTACATTTGAAT 1140

QY 1141 ACAGTGCAGCTTAGTAAACTGTTGCAAGAAATGTCGCTCATATGAAAGAGATCCTGG 1200
DB 1141 ACAGTGCAGCTTAGTAAACTGTTGCAAGAAATGTCGCTCATATGAAAGAGATCCTGG 1200

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DB 1201 TTTGAGCAGTTTAAATGTCGAAAGATTCGATGGAACTGGATGGAACTGGATCTGACTGGAG 1260

QY 1261 GAAAGCAATTCAGAAAGTCTTATCAACCTGGCTCCAAAGTTCTCAGGAGTACCTGGAT 1320
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QY 1321 GCTCTGAAGAGCTGAGCTTGTCTTCTGAGTGCAAGTGGGCCAGTTCTACCCCTGCTCC 1380
DB 1321 GCTCTGAAGAGCTGAGCTTGTCTTCTGAGTGCAAGTGGGCCAGTTCTACCCCTGCTCC 1380

QY 1381 TGCTCAGCGTCCCAAGGACCTGCACAGAAAGGCTGAGCTGGAAGTCCCACTGTCTCATCTC 1440
DB 1381 TGCTCAGCGTCCCAAGGACCTGCACAGAAAGGCTGAGCTGGAAGTCCCACTGTCTCATCTC 1440

QY 1441 CTGGGTTTCTCTCTCTTTTATTTGGTATCTCTGGTTCTTTTCGGCCGCTTCAAGTCTG 1500
DB 1441 CTGGGTTTCTCTCTCTTTTATTTGGTATCTCTGGTTCTTTTCGGCCGCTTCAAGTCTG 1500

QY 1501 TGTGCACTCAGCTGAAAGTTCGCTGCTTCTGCTGGCTCTCTGCTGGCTGGCGGAGGCT 1560
DB 1501 TGTGCACTCAGCTGAAAGTTCGCTGCTTCTGCTGGCTCTCTGCTGGCTGGCGGAGGCT 1560

QY 1561 GCCTTTCTGTTTACAGACTCTGTTGAAACCTGCTGTGTGCCAAGTGTCTGCGAGTGCCC 1620
DB 1561 GCCTTTCTGTTTACAGACTCTGTTGAAACCTGCTGTGTGCCAAGTGTCTGCGAGTGCCC 1620

QY 1621 TGGACAGGGGCTCAGGGAAGGACGTTGGAGAGCCTTATCCAGGCTCTGGGTGTCCC 1680
DB 1621 TGGACAGGGGCTCAGGGAAGGACGTTGGAGAGCCTTATCCAGGCTCTGGGTGTCCC 1680

QY 1681 GACACAGTGTTCACATCTGCTGTCAGGTGATGCTCAGTCTTCTTGGAAAGCTAGT 1740
DB 1681 GACACAGTGTTCACATCTGCTGTCAGGTGATGCTCAGTCTTCTTGGAAAGCTAGT 1740

QY 1741 TCCTGCGACTGTTTACCAAGTGTGTTAAAGAGCTGCGGTTCACAGAGGACAGCCCCC 1800
DB 1741 TCCTGCGACTGTTTACCAAGTGTGTTAAAGAGCTGCGGTTCACAGAGGACAGCCCCC 1800

1801 CAGCTGAGGGGGTGTGTGAATCGACACAGCTCCAGCAGAGGTTGGGAGCTGCAGCTGA 1860
1801 CAGCTGAGGGGGTGTGTGAATCGACACAGCTCCAGCAGAGGTTGGGAGCTGCAGCTGA 1860
1861 GGGAGAGAGACAAATCGGCTGGACACTCAGGAGGGTCAAAAGGAGACTTGGTGCAC 1920
1861 GGGAGAGAGACAAATCGGCTGGACACTCAGGAGGGTCAAAAGGAGACTTGGTGCAC 1920
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1921 ACTCATCTCGCCACCCAGAAATCATCTGCTCATCAGGTCAGATTTCTTCCAGG 1980
1981 CGGAGTTTCTGTGGAATCTTAGTCTTGGCTCGACACCTTCATGTTAGTGG 2040
1981 CGGAGTTTCTGTGGAATCTTAGTCTTGGCTCGACACCTTCATGTTAGTGG 2040
2041 GGAGTGTGTGAGGAGTGAAGAGAGGCGGATGCTCACACTCAGATCCACAGAGCCCA 2100
2041 GGAGTGTGTGAGGAGTGAAGAGAGGCGGATGCTCACACTCAGATCCACAGAGCCCA 2100
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2101 GGATCAAGGGACCCACTCGAGTGGCAGCAGGACTGTGGGCCCCCACCACCCCTGCAC 2160
2161 AGCCCTCATCCCTCTTGGCTTGGCGTGCAGAGGCGCTGTGCTGAGTGTCTGACCGAGA 2220
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2221 CACTCACAGCTTGTGATCAGGGGCAAGGCTTCTCGGAGCCAGGATGATCTGTGCCAG 2280
2281 CTTGCACTCGGGCCCATCTGGGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
2281 CTTGCACTCGGGCCCATCTGGGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
2341 CTGCAACAGTATGTAGTTACCAAAAGATAAAGCGCAATAATTGAGAAAAA 2395
2341 CTGCAACAGTATGTAGTTACCAAAAGATAAAGCGCAATAATTGAGAAAAA 2395

RESULT 3
AAF92127
ID AAF92127 standard; cDNA; 2395 BP.
XX
AC AAF92127;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO4405 cDNA.
XX
KW Human; PRO protein; mapping; ss.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US023328.
XX
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR

25-APR-2000; 2000US-0199397P.
22-MAY-2000; 2000WO-US014042.
05-JUN-2000; 2000US-0209832P.
PA (GETH) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen MB, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2001-183260/18.
DR P-FSDB; AAB87595.
XX
PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX
XX Claim 2; Fig 139; 278pp; English.
XX
PS The present sequence is the coding sequence for a human PRO polypeptide
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC antagonists or anti-PRO antibodies are useful for preparation of a
CC medicament useful in the treatment of a condition which is responsive to
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping
XX
SQ Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;
Query Match 100.0%; Score 2395; DB 4; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGAGCGGAGCGGCTGCAGCAGGCGGAGCTCCAGGTGGGGTCCGTTCCGCATC 60
DB 1 CCTGGAGCGGAGCGGCTGCAGCAGGCGGAGCTCCAGGTGGGGTCCGTTCCGCATC 60
QY 61 CAGCCTTAGCGTGTCCACGATGCGGTGGCTCGGACCTTTTCGTTACCTGTTCCGTAGCG 120
DB 61 CAGCCTTAGCGTGTCCACGATGCGGTGGCTCGGACCTTTTCGTTACCTGTTCCGTAGCG 120
QY 121 ATCGAGGTGCTAGGATCGGCTCTTCTTCCGCGGATCTTCCCGGCTCCGTTCTTC 180
DB 121 ATCGAGGTGCTAGGATCGGCTCTTCTTCCGCGGATCTTCCCGGCTCCGTTCTTC 180
QY 181 TCTGCCAGAGCGAACAACAGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 240
DB 181 TCTGCCAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 240
QY 241 TCTAACTGGACCACTGCGCACCACTCTCTTTCAGTAAAGTTGTTATTTCTGTATAGAT 300
DB 241 TCTAACTGGACCACTGCGCACCACTCTCTTTCAGTAAAGTTGTTATTTCTGTATAGAT 300
QY 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAGGCTGTAAGTTTATGCGCTTACCAACT 360
DB 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAGGCTGTAAGTTTATGCGCTTACCAACT 360
QY 361 TACCTTGTGAAAAAGGAGCATCTCAGATTTTGTGGCTGAAGCAAGCAAGCAAGCAAGT 420
DB 361 TACCTTGTGAAAAAGGAGCATCTCAGATTTTGTGGCTGAAGCAAGCAAGCAAGT 420
QY 421 ACTATGCTCGAATCAAGGATGATGACGGGAGCGCTTCTGCGTTCGAGTTCATC 480
DB 421 ACTATGCTCGAATCAAGGATGATGACGGGAGCGCTTCTGCGTTCGAGTTCATC 480
QY 481 AGGAACCTCAATTTCTCTCGACACTGCTGGAAGACAGTGTGATAGCAAGCAAGCAAGT 540
DB 481 AGGAACCTCAATTTCTCTCGACACTGCTGGAAGACAGTGTGATAGCAAGCAAGCAAGT 540
QY 541 GGAAAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTTATTCCTCCAAAGCATTTT 600
DB 541 GGAAAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTTATTCCTCCAAAGCATTTT 600

QY	601	GTGAAATATGATGGAAACAACCTCATTTTTCGTGTGTCAGATTACACAGAGGTGGATAATAAT	660
Db	601	GTGAAATATGATGGAAACAACCTCATTTTTCGTGTGTCAGATTACACAGAGGTGGATAATAAT	660
QY	661	GTCCAGGAGCATTTGGATAAGTATTAAGAGAGGAGATTGGGACATATTAATCCTCCAC	720
Db	661	GTCCAGGAGCATTTGGATAAGTATTAAGAGAGGAGATTGGGACATATTAATCCTCCAC	720
QY	721	TACCTGGGCTGGACCAACATTTGGCCACATTTACGGGCCCAACAGCCCTGATTTGGGCAG	780
Db	721	TACCTGGGCTGGACCAACATTTGGCCACATTTACGGGCCCAACAGCCCTGATTTGGGCAG	780
QY	781	AAGCTGAGCGAGATGACAGCGTGTCTGATGAAGATCCACACCTCAGTCGAGTGAAGGAG	840
Db	781	AAGCTGAGCGAGATGACAGCGTGTCTGATGAAGATCCACACCTCAGTCGAGTGAAGGAG	840
QY	841	AGAGAGACGCTTTTACCCAAATTTGCTGTCTTTTGTGTGTCGACCATGGCATGCTGAACA	900
Db	841	AGAGAGACGCTTTTACCCAAATTTGCTGTCTTTTGTGTGTCGACCATGGCATGCTGAACA	900
QY	901	GGAAAGTCAAGGGGCTCTCTCCACCGAGAGGTGAATAACCTCTGTGATTTTAAATCAGTTCT	960
Db	901	GGAAAGTCAAGGGGCTCTCTCCACCGAGAGGTGAATAACCTCTGTGATTTTAAATCAGTTCT	960
QY	961	GCCTTTGAAGGAACACCGGTGATATCCGACATCCAAAGCACGTCGAATAGACGGATGTG	1020
Db	961	GCCTTTGAAGGAACACCGGTGATATCCGACATCCAAAGCACGTCGAATAGACGGATGTG	1020
QY	1021	GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCTCAAGACAGCTGAGGAGGCTC	1080
Db	1021	GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCTCAAGACAGCTGAGGAGGCTC	1080
QY	1081	CTATTCCTCCAGTTGTGAAGGAAGACCAATCAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
Db	1081	CTATTCCTCCAGTTGTGAAGGAAGACCAATCAGAGAGCAGTTGAGATTTTACATTTGAAT	1140
QY	1141	ACAGTCAGCTTAGTAAACTGTTGCAAGAAATGTGCCGTATATGAAGAAAGATTCCTGGG	1200
Db	1141	ACAGTCAGCTTAGTAAACTGTTGCAAGAAATGTGCCGTATATGAAGAAAGATTCCTGGG	1200
QY	1201	TTTGACAGCTTTAAATGTTCAGAAAGATTGCATGGGAACCTGGATCAGACTGTACTTGGAG	1260
Db	1201	TTTGACAGCTTTAAATGTTCAGAAAGATTGCATGGGAACCTGGATCAGACTGTACTTGGAG	1260
QY	1261	GAAAGCATTCAGAGTCTTATTAACCTGGGCTCCAAGGTTCTCAGGCAAGTACCTGGAT	1320
Db	1261	GAAAGCATTCAGAGTCTTATTAACCTGGGCTCCAAGGTTCTCAGGCAAGTACCTGGAT	1320
QY	1321	GCTCTGAAGACGCTGAGCTGTCTCCCTGAGTGCACAAGTGGCCCAAGTTCTCACCTGCTCC	1380
Db	1321	GCTCTGAAGACGCTGAGCTGTCTCCCTGAGTGCACAAGTGGCCCAAGTTCTCACCTGCTCC	1380
QY	1381	TGCTCAGCGTCCACAGGCACTGCACAGAAAGCTCAGCTGGAAAGTCCCACTGTCACTC	1440
Db	1381	TGCTCAGCGTCCACAGGCACTGCACAGAAAGCTCAGCTGGAAAGTCCCACTGTCACTC	1440
QY	1441	CTGGGTTTCTCTGCTCTTTTATTTGGTGAATCTGTTCTTTCCGCCGTTCAAGTCAATTG	1500
Db	1441	CTGGGTTTCTCTGCTCTTTTATTTGGTGAATCTGTTCTTTCCGCCGTTCAAGTCAATTG	1500
QY	1501	TGTGCACCTCAGCTGAAGTCTGTCTACTTCTGTGGCCTCTGTGGCTGGCGGAGGCT	1560
Db	1501	TGTGCACCTCAGCTGAAGTCTGTCTACTTCTGTGGCCTCTGTGGCTGGCGGAGGCT	1560
QY	1561	GCCTTTCTGTTTACAGACTCTGTGTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCC	1620
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QY	1621	TGGAAGGGGGCTCAGGGAAGGACGTGGAGCAGCTTATCCAGGCTCTGGGTGCTCC	1680
Db	1621	TGGAAGGGGGCTCAGGGAAGGACGTGGAGCAGCTTATCCAGGCTCTGGGTGCTCC	1680

QY	1681	GACACAGCTTTTCAATCTGTGTGTCTAGGTCCAGATCCCTCAGTTCTTGAAAGCTAGGT	1740
Db	1681	GACACAGCTTTTCAATCTGTGTGTCTAGGTCCAGATCCCTCAGTTCTTGAAAGCTAGGT	1740
QY	1741	TCCTGGGACTTTTACCAAGGTGATTGTAAAGAGCTGCGGTCAAGAGGAAAGAGCCCC	1800
Db	1741	TCCTGGGACTTTTACCAAGGTGATTGTAAAGAGCTGCGGTCAAGAGGAAAGAGCCCC	1800
QY	1801	CAGCTGAGGGGTGTGTGAATCGGACAGCTCCAGCAGAGGTGTGGAGCTGACGTGA	1860
Db	1801	CAGCTGAGGGGTGTGTGAATCGGACAGCTCCAGCAGAGGTGTGGAGCTGACGTGA	1860
QY	1861	GGGAAGAAGAGACAATCGGCTGAGCACTCAGAGGGTCAAAAGGAGACTTGTGCGACC	1920
Db	1861	GGGAAGAAGAGACAATCGGCTGAGCACTCAGAGGGTCAAAAGGAGACTTGTGCGACC	1920
QY	1921	ACTCATCTCCGACCCCAAGATTCATCTCCCTCATCAGGTCCAGATTTCTTCCAAAG	1980
Db	1921	ACTCATCTCCGACCCCAAGATTCATCTCCCTCATCAGGTCCAGATTTCTTCCAAAG	1980
QY	1981	CGGACGTTTTCTGTGGAATTTCTTAGTCTTGGCTCGGACACCTTCATTCTGTAGCTGG	2040
Db	1981	CGGACGTTTTCTGTGGAATTTCTTAGTCTTGGCTCGGACACCTTCATTCTGTAGCTGG	2040
QY	2041	GGAGTGTGTGAGGAGTGAAGAAGGCGGATGTCACACTCAGATCCACAGAGCCCA	2100
Db	2041	GGAGTGTGTGAGGAGTGAAGAAGGCGGATGTCACACTCAGATCCACAGAGCCCA	2100
QY	2101	GGATCAAGGACCCACTGCACTGGCAGGAGCTGTGGGCCCCCACCACCCCTGCAC	2160
Db	2101	GGATCAAGGACCCACTGCACTGGCAGGAGCTGTGGGCCCCCACCACCCCTGCAC	2160
QY	2161	AGCCCTCATCCCTCTTGGCTTCAGCCGTTCAGAGGCCCTGTGTGAGTCTGACCGAGA	2220
Db	2161	AGCCCTCATCCCTCTTGGCTTCAGCCGTTCAGAGGCCCTGTGTGAGTCTGACCGAGA	2220
QY	2221	CACCTCAGCTTTGTTCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACG	2280
Db	2221	CACCTCAGCTTTGTTCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACG	2280
QY	2281	CTTGACCTCGGGCCCATCTGGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2340
Db	2281	CTTGACCTCGGGCCCATCTGGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2340
QY	2341	CTGCACACATGTAGTTTACCAAAAGATTAACGGCAATTAATTGAGAAAAAAA	2395
Db	2341	CTGCACACATGTAGTTTACCAAAAGATTAACGGCAATTAATTGAGAAAAAAA	2395

RESULT 4
AAC91490
ID AAC91490 standard; cDNA; 2395 BP.
XX AAC91490;
AC AAC91490;
XX 21-MAR-2001 (first entry)
DT Human PRO4405 cDNA.
DE Human; PRO; antiinflammatory; dermatological; antiarthritic;
XX antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW antiallergic; antiasthmatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy; ss.
XX Homo sapiens.
OS
XX
XX WO200073452-A2.
PN
XX
XX 07-DEC-2000.
PD
XX
XX 02-JUN-2000; 2000WO-US015264.
PF
XX

		Query Match		100.0%; Score 2395; DB 5; Length 2395;		Best Local Similarity 100.0%; Pred. No. 0;		Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
PR	02-JUN-1999;	99WO-US012252.							
PR	20-JUL-1999;	99US-0144732P.							
PR	20-JUL-1999;	99US-0144758P.							
PR	28-JUL-1999;	99US-0146222P.							
PR	01-SEP-1999;	99WO-US020111.							
PR	15-SEP-1999;	99WO-US021090.							
PR	15-SEP-1999;	99WO-US021547.							
PR	29-OCT-1999;	99US-0162506P.							
PR	30-NOV-1999;	99WO-US028313.							
PR	01-DEC-1999;	99WO-US028634.							
PR	02-DEC-1999;	99WO-US028551.							
PR	02-DEC-1999;	99WO-US028565.							
PR	09-DEC-1999;	99US-0170262P.							
PR	20-DEC-1999;	99WO-US030911.							
PR	05-JAN-2000;	2000WO-US000219.							
PR	06-JAN-2000;	2000WO-US000376.							
PR	11-FEB-2000;	2000WO-US003565.							
PR	18-FEB-2000;	2000WO-US004341.							
PR	18-FEB-2000;	2000WO-US004342.							
PR	24-FEB-2000;	2000WO-US004414.							
PR	24-FEB-2000;	2000WO-US004914.							
PR	01-MAR-2000;	2000WO-US005601.							
PR	02-MAR-2000;	2000WO-US005841.							
PR	03-MAR-2000;	2000US-0187202P.							
PR	15-MAR-2000;	2000WO-US006884.							
PR	20-MAR-2000;	2000WO-US007377.							
PR	21-MAR-2000;	2000WO-US007532.							
PR	30-MAR-2000;	2000WO-US008439.							
PR	17-MAY-2000;	2000WO-US013705.							
PR	22-MAY-2000;	2000WO-US014042.							
XX									
PA	(GETH) GENENTECH INC.								
XX									
XX	Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ;								
PI	Gurney AL, Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D;								
PI	Watanabe CK, Wood WI;								
XX									
DR	WPI; 2001-025253/03.								
DR	P-PSDB; AAB50931.								
XX									
PT	Thirty three nucleic acids encoding PRO polypeptides which are useful in								
PT	the diagnosis and treatment of immune related disorders, e.g. systemic								
PT	lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis								
PT	and diabetes mellitus.								
XX									
PS	Claim 48; Fig 59; 218pp; English.								
XX									
CC	The present sequence is one of thirty three nucleic acids encoding PRO								
CC	polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and								
CC	antagonists are useful for treating and diagnosing immune related								
CC	disorders such as systemic lupus erythematosus, rheumatoid arthritis,								
CC	osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,								
CC	systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's								
CC	syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic								
CC	anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,								
CC	immune-mediated renal disease, demyelinating diseases of the central and								
CC	peripheral nervous systems (such as multiple sclerosis, idiopathic								
CC	demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic								
CC	inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such								
CC	as infectious, autoimmune chronic active hepatitis, primary biliary								
CC	cirrhosis, granulomatous hepatitis and sclerosing cholangitis),								
CC	inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's								
CC	disease, autoimmune or immune-mediated skin diseases (such as bullous								
CC	skin diseases, erythema multiforme, contact dermatitis, psoriasis),								
CC	allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,								
CC	food hypersensitivity and urticaria), immunological diseases of the lung								
CC	(such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and								
CC	hypersensitivity pneumonitis), transplantation associated diseases								
CC	including graft rejection and graft-versus-host diseases								
XX									
SQ	Sequence 2395 BP; 566 A; 605 C; 656 G; 569 T; 0 U; 0 Other;								

DR	WPI; 2002-172001/22.	QY	601	GTGGAATATGATGGAAACAACTCTATTTTCGTGTGATATACACAGAGGTGGATAAT	660
DR	P-PSDB; AAU83650.	DB	601	GTGGAATATGATGGAAACAACTCTATTTTCGTGTGATATACACAGAGGTGGATAAT	660
XX					
PT	One hundred and twenty two nucleic acids encoding PRO polypeptides,	QY	661	GTACACAGGCAATTTGATTAAGTATTAAAGAGGAGATTGGACATATTAAATCTCCAC	720
PT	useful for treating a PRO related disorder and for diagnosing tumors such	DB	661	GTACACAGGCAATTTGATTAAGTATTAAAGAGGAGATTGGACATATTAAATCTCCAC	720
PT	as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor				
PT	or liver tumor.				
XX					
PS	Claim 2; Fig 117; 359pp; English.	QY	721	TACTCGGGCTGACCAACATTTGGCCACATTTAGGGCCCAACAGCCCCCTGATTTGGGAG	780
PS		DB	721	TACTCGGGCTGACCAACATTTGGCCACATTTAGGGCCCAACAGCCCCCTGATTTGGGAG	780
XX					
CC	The invention relates to one hundred and twenty two nucleic acids	QY	781	AACTCAGCGAGATGAGACGCTGCTGATGAAGATCCACCTCAGTGCAGTGAAGGAG	840
CC	encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides	DB	781	AACTCAGCGAGATGAGACGCTGCTGATGAAGATCCACCTCAGTGCAGTGAAGGAG	840
CC	encode human secreted proteins. The PRO nucleic acids, polypeptides,				
CC	agonists and antagonists are useful for treating a PRO related disorder.				
CC	The PRO polypeptides are useful for diagnosing tumours, especially lung				
CC	cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or				
CC	liver tumour. The PRO polypeptides are useful for stimulating the				
CC	proliferation of, or gene expression, in pericyte cells, for stimulating	QY	841	AGAGAGCGCTTTACCCAAATTTGCTGTTTCTTTGCTGACCATGCGCATGTCTGAACA	900
CC	the proliferation or differentiation of chondrocyte cells, for	DB	841	AGAGAGCGCTTTACCCAAATTTGCTGTTTCTTTGCTGACCATGCGCATGTCTGAACA	900
CC	stimulating the release of tumour necrosis factor-alpha from human blood,	QY	901	GGAAGTCACGGGGCTCTCCACCGAGGAGTGAATACACCTCTGATTTTAAATCAGTTCT	960
CC	for stimulating or inhibiting the proliferation of normal human dermal	DB	901	GGAAGTCACGGGGCTCTCTCCACCGAGGAGTGAATACACCTCTGATTTTAAATCAGTTCT	960
CC	fibroblast cells. The PRO polypeptide may also be used as molecular				
CC	weight markers and for tissue typing. The PRO nucleic acids have	QY	961	GCGTTTCAAGAGAAACCCGGTGATATCCGACATCCAAAGCACGCTCCAAATAGCCGATGTG	1020
CC	applications in molecular biology, including use as hybridisation probes,	DB	961	GCGTTTCAAGAGAAACCCGGTGATATCCGACATCCAAAGCACGCTCCAAATAGCCGATGTG	1020
CC	and in chromosome and gene mapping. ABK33536-ABK33657 represent human PRO				
CC	protein coding sequences of the invention				
XX					
SQ	Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;	QY	1021	GCTCGGACATCGGCGATAGACATTTGGCTTACCGGATTCCTCAAGAGACAGTGTAGGAGGCTC	1080
	Query Match 100.0%; Score 2395; DB 6; Length 2395;	DB	1021	GCTCGGACATCGGCGATAGACATTTGGCTTACCGGATTCCTCAAGAGACAGTGTAGGAGGCTC	1080
	Best Local Similarity 100.0%; Pred. No. 0;				
	Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY	1081	CTATTCCAGTGTGGAGGAAGAACCAATGAGAGAGAGTGTGAGATTTTACATTTGAAT	1140
		DB	1081	CTATTCCAGTGTGGAGGAAGAACCAATGAGAGAGAGTGTGAGATTTTACATTTGAAT	1140
QY	1 CCTCGAGCGGAAGCGGCTGACAGCGGCGAGGCTCCAGGTGGGTTCGGTTCGCAATC 60	QY	1141	ACAGTGCAGCTTAAACTCTGTTGCAAGAGAAATGTGCGGTATATGAAAGAGATCTCTGGG	1200
DB	1 CCTGAGCGGAGAGCGGCTGACAGCGGCGAGGCTCCAGGTGGGTTCGGTTCGCAATC 60	DB	1141	ACAGTGCAGCTTAAACTCTGTTGCAAGAGAAATGTGCGGTATATGAAAGAGATCTCTGGG	1200
QY	61 CAGCTAGCTGTCCAGATCGGCTCGGACTTCGGGACTTTCCGCTGCTGCTGCTGCTG 120	QY	1201	TTTGAGCAGTGTAAATGTCAAGAAAGATTGATGGAACTGGATGGAATCTGTACTTGGAG	1260
DB	61 CAGCTAGCTGTCCAGATCGGCTCGGACTTCGGGACTTTCCGCTGCTGCTGCTGCTG 120	DB	1201	TTTGAGCAGTGTAAATGTCAAGAAAGATTGATGGAACTGGATGGAATCTGTACTTGGAG	1260
QY	121 ATCGAGGTGTAGGATCGGCTCTCTTCGGGGATTTCTTCCGGCTCCCGTTCGTTCC 180	QY	1261	GAAAGCAATTCAGAGTCTCTATTCAACCTGGGCTCAAAGTTCCTCAGGAGTACCTGGAT	1320
DB	121 ATCGAGGTGTAGGATCGGCTCTCTTCGGGGATTTCTTCCGGCTCCCGTTCGTTCC 180	DB	1261	GAAAGCAATTCAGAGTCTCTATTCAACCTGGGCTCAAAGTTCCTCAGGAGTACCTGGAT	1320
QY	181 TCTGCGAGCGGAACACGAGCGGAGCCCGAGCCCGGAGCCCTCGGCTGGAGCCAGT 240	QY	1321	GCTCTGAAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCCACTTCTCACCCCTGCTCC	1380
DB	181 TCTGCGAGCGGAACACGAGCGGAGCCCGAGCCCGGAGCCCTCGGCTGGAGCCAGT 240	DB	1321	GCTCTGAAAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCCACTTCTCACCCCTGCTCC	1380
QY	241 TCTAACTGACACGCTGCCACCACTCTCTTCAAGTAAAGTGTATTGTTCTGATAGAT 300	QY	1381	TGCTCAGCGTCCACAGGCACTGACAGAAAGGCTGAGCTGGAAGTCCCACTGTCTATCTC	1440
DB	241 TCTAACTGACACGCTGCCACCACTCTCTTCAAGTAAAGTGTATTGTTCTGATAGAT 300	DB	1381	TGCTCAGCGTCCACAGGCACTGACAGAAAGGCTGAGCTGGAAGTCCCACTGTCTATCTC	1440
QY	301 GCCTTGAGAGATGATTTGTTGGGTCAAAAGGTTGTGAATTTATGCCCTACACAACT 360	QY	1441	CTGGGTTTCTCTGCTCTTTTATTTTGGTGAATCCTGGTTCCTTGGGCGGTTTACGTCATTTG	1500
DB	301 GCCTTGAGAGATGATTTGTTGGGTCAAAAGGTTGTGAATTTATGCCCTACACAACT 360	DB	1441	CTGGGTTTCTCTGCTCTTTTATTTTGGTGAATCCTGGTTCCTTGGGCGGTTTACGTCATTTG	1500
QY	361 TACCTTGTGGAAGAGGAGCACTCTCAAGTTTGTGGCTGGAAGCAAGCCACTCAGTT 420	QY	1501	TGTGACCTCAGCTGAAAGTTCGTCTACTTCTGTGGCTCTCTGTGGCTGGCGGAGGCT	1560
DB	361 TACCTTGTGGAAGAGGAGCACTCTCAAGTTTGTGGCTGGAAGCAAGCCACTCAGTT 420	DB	1501	TGTGACCTCAGCTGAAAGTTCGTCTACTTCTGTGGCTCTCTGTGGCTGGCGGAGGCT	1560
QY	421 ACTATGCTCGAATCAAGCAATGATGACGGGAGGCTTCTTGGCTTGTGACGCTCATC 480	QY	1561	GCCTTTCGTTTACCAGACTCTGTTGAAACACCTGGTGTGCAAGTGTGGCAGTGGCC	1620
DB	421 ACTATGCTCGAATCAAGCAATGATGACGGGAGGCTTCTTGGCTTGTGACGCTCATC 480	DB	1561	GCCTTTCGTTTACCAGACTCTGTTGAAACACCTGGTGTGCAAGTGTGGCAGTGGCC	1620
QY	481 AGGAACCTCAATCTCCTGCACTGCTGGAAGCAGTGTGATAGACAAGCAAGCAGCT 540	QY	1621	TGGACAGGGGGCTCAGGAAAGCACTGTGAGAGACCTTATCCAGGCTCTGGGTCTCC	1680
DB	481 AGGAACCTCAATCTCCTGCACTGCTGGAAGCAGTGTGATAGACAAGCAAGCAGCT 540	DB	1621	TGGACAGGGGGCTCAGGAAAGCACTGTGAGAGACCTTATCCAGGCTCTGGGTCTCC	1680
QY	541 GGAAGAAAGATAGCTCTTTATGAGATGAACCTGGGTAAATTTATCCCAAGCAATTT 600	QY	1681	GACACAGGTGTTACACATCTGTGCTGTCAGTGCAGTGCCTCAGTTCTTGTGAAAGTAGGT	1740
DB	541 GGAAGAAAGATAGCTCTTTATGAGATGAACCTGGGTAAATTTATCCCAAGCAATTT 600	DB	1681	GACACAGGTGTTACACATCTGTGCTGTCAGTGCAGTGCCTCAGTTCTTGTGAAAGTAGGT	1740

Fri Aug 6 10:49:39 2004

09-JUL-2001; 2001WO-US021735.
(GETH) GENENTECH INC.
Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
WPI; 2002-731348/79.
P-PSDB; ABG95920.
XX New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX Claim 2; Fig 139; 399pp; English.
XX The invention relates to an isolated secreted and transmembrane PRO
XX polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, C/G, D/H or E/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO3801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I. The antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
XX invention
SQ Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;
Query Match 100.0%; Score 2395; DB 6; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGAGCGGAGCGCGCTCGACAGGCGGAGGCTCAGGTGGGTCGGTCCGCATC 60
DB 1 CCTGGAGCGGAGCGCGCTCGACAGGCGGAGGCTCAGGTGGGTCGGTCCGCATC 60
QY 61 CAGCCTAGCGTGTCCACAGTGGGCTCGGCTCGGACCTTCGTACCTCTGTCGCTAGCG 120
DB 61 CAGCCTAGCGTGTCCACAGTGGGCTCGGCTCGGACCTTCGTACCTCTGTCGCTAGCG 120
QY 121 ATCGAGGTGTAGGAGTGGCGTCTTCTTCTTGGGAGTCTTCCCGCTCCCGTCTGTTCC 180

Db 121 ATCGAGGTGTAGGAGTGGCGTCTTCTTCTTGGGAGTCTTCCCGCTCCCGTCTGTTCC 180
QY 181 TCTGCGCAGAGCGGAGAACACGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 240
DB 181 TCTGCGCAGAGCGGAGAACACGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 240
QY 241 TCTAACTGGACACCGCTGCCACACCTCTCTCTTCACTAAAGTTGTTATTTCTGATAGAT 300
DB 241 TCTAACTGGACACCGCTGCCACACCTCTCTCTTCACTAAAGTTGTTATTTCTGATAGAT 300
QY 301 GCGTTGAGAGATGATTTTGTGTTGGTCAAGGGTGAATTTTATGCCCTACACAACCT 360
DB 301 GCGTTGAGAGATGATTTTGTGTTGGTCAAGGGTGAATTTTATGCCCTACACAACCT 360
QY 361 TACCTTTGCGAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCAAGCAAGCAAGTT 420
DB 361 TACCTTTGCGAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCAAGCAAGCAAGTT 420
QY 421 ACTATGCTCGAATCAAGGCAATGATGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 480
DB 421 ACTATGCTCGAATCAAGGCAATGATGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 480
QY 481 AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAGACAGCAAGCAAGCAAG 540
DB 481 AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAGACAGCAAGCAAGCAAG 540
QY 541 GGAAGAAGATAGTCTTTTATGAGATGAACCTGGGTAAATTTATTTCCCAAGCAATTTT 600
DB 541 GGAAGAAGATAGTCTTTTATGAGATGAACCTGGGTAAATTTATTTCCCAAGCAATTTT 600
QY 601 GTGGAATATGATGAACCAACCTCAATTTTGTGTCAGATACACAGAGGTGGATTAAT 660
DB 601 GTGGAATATGATGAACCAACCTCAATTTTGTGTCAGATACACAGAGGTGGATTAAT 660
QY 661 GTGGAAGGATTTGGATTAAGTATTAAGAGGAGATGGGACATATTAATCTCCAC 720
DB 661 GTGGAAGGATTTGGATTAAGTATTAAGAGGAGATGGGACATATTAATCTCCAC 720
QY 721 TACCTGGGCTGGACCACTATGGCCACATTTTCAGGCGCCCAACAGCCCTGATTTGGGAG 780
DB 721 TACCTGGGCTGGACCACTATGGCCACATTTTCAGGCGCCCAACAGCCCTGATTTGGGAG 780
QY 781 AAGTGTGCGAGATGAGCAGCGTCTGATGAAGTCCACACCTCACTGAGTCCGAGGAG 840
DB 781 AAGTGTGCGAGATGAGCAGCGTCTGATGAAGTCCACACCTCACTGAGTCCGAGGAG 840
QY 841 AGAGAGCGCTTTTACCCCAATTTGCTGTTCTTTGTGTCGATGAGGATGCTGAAACA 900
DB 841 AGAGAGCGCTTTTACCCCAATTTGCTGTTCTTTGTGTCGATGAGGATGCTGAAACA 900
QY 901 GGAAGTCAAGGCGGCTCTCCACCGAGGAGTGAATACACCTCTGATTTTATTCAGTTCT 960
DB 901 GGAAGTCAAGGCGGCTCTCTCCACCGAGGAGTGAATACACCTCTGATTTTATTCAGTTCT 960
QY 961 GCGTTTGAAGAGAAACCGGTCGATATCCGACATCCAAAGCAGCTCCCAATAGACGATG 1020
DB 961 GCGTTTGAAGAGAAACCGGTCGATATCCGACATCCAAAGCAGCTCCCAATAGACGATG 1020
QY 1021 GCTGCGACATCGCGATAGCACTTGGCTTTACCGATTTCCAAAAGACAGATGTAGGGAGCT 1080
DB 1021 GCTGCGACATCGCGATAGCACTTGGCTTTACCGATTTCCAAAAGACAGATGTAGGGAGCT 1080
QY 1081 CTATTTCCCAAGTGTGGAAGGAAAGCAATGAGAGAGCAGTTCAGATTTTATTCAGTT 1140
DB 1081 CTATTTCCCAAGTGTGGAAGGAAAGCAATGAGAGAGCAGTTCAGATTTTATTCAGTT 1140
QY 1141 ACAGTGCAGCTTAGTAAACCTGTTGCAAGAGATGTCCTCATATGAAAAAGATCTCGG 1200
DB 1141 ACAGTGCAGCTTAGTAAACCTGTTGCAAGAGATGTCCTCATATGAAAAAGATCTCGG 1200
QY 1201 TTTGAGCAGTTTAAAATGTGAGAAAGATTCAGATGAGAACTGGATCAGATCTACTTGGAG 1260

Db 1201 TTTCAGCAGTTTAAATGTCAGAAAGATTGTCATGGAACTGGATCAGACTGCTACTGGAG 1260

Qy 1261 GAAAGCAATTCAGAGTCCTATTCAACTGGGCTCCAAAGTTTCAGGCACTGACTGAT 1320

Db 1261 GAAAGCAATTCAGAGTCCTATTCAACTGGGCTCCAAAGTTTCAGGCACTGACTGAT 1320

Qy 1321 GCTCTGAAGACGCTGAGCTTCTCCTCAGTGCCACAGTGGCCCACTTCTCACTGCTCC 1380

Db 1321 GCTCTGAAGACGCTGAGCTTCTCCTCAGTGCCACAGTGGCCCACTTCTCACTGCTCC 1380

Qy 1381 TGCTCAGGCTCCACAGGCACTGACAGAAAGGCTGAGCTGGAAGTCCCACTGCTCCTC 1440

Db 1381 TGCTCAGGCTCCACAGGCACTGACAGAAAGGCTGAGCTGGAAGTCCCACTGCTCCTC 1440

Qy 1441 CTGGGTTTCTCTGCTCTTTTATTGTTGATCTGCTGTTCTTTCGGCGGTTCACTGCTAT 1500

Db 1441 CTGGGTTTCTCTGCTCTTTTATTGTTGATCTGCTGTTCTTTCGGCGGTTCACTGCTAT 1500

Qy 1501 TGTGCACTCAGCTGAAAGTTCTGCTACTTCTGTCGCTCTGCTGCTGCTGCTGCTGCT 1560

Db 1501 TGTGCACTCAGCTGAAAGTTCTGCTACTTCTGTCGCTCTGCTGCTGCTGCTGCTGCT 1560

Qy 1561 GCCTTCTGTTTACAGACTCTGCTGTTGAACACCTGCTGTTGCTGCTGCTGCTGCTGCT 1620

Db 1561 GCCTTCTGTTTACAGACTCTGCTGTTGAACACCTGCTGTTGCTGCTGCTGCTGCTGCT 1620

Qy 1621 TGGACAGGGGGCTCAGGAGGAGCTGAGAGGCTTATCCAGGCTCTGCTGCTGCTGCT 1680

Db 1621 TGGACAGGGGGCTCAGGAGGAGCTGAGAGGCTTATCCAGGCTCTGCTGCTGCTGCT 1680

Qy 1681 GACACAGGCTTTCACATCTGCTGCTCAGTCTGATGCTGCTGCTGCTGCTGCTGCTGCT 1740

Db 1681 GACACAGGCTTTCACATCTGCTGCTCAGTCTGATGCTGCTGCTGCTGCTGCTGCTGCT 1740

Qy 1741 TCTGCGACTGTTTACCAAGTGTATGTAAGAGCTGCGGCTCAGAGGAAACAGCCCTC 1800

Db 1741 TCTGCGACTGTTTACCAAGTGTATGTAAGAGCTGCGGCTCAGAGGAAACAGCCCTC 1800

Qy 1801 CAGCTCAGGGGGTGTGATTCGACAGCTTCCAGGAGGCTGAGGAGCTGAGGAGCTGAG 1860

Db 1801 CAGCTCAGGGGGTGTGATTCGACAGCTTCCAGGAGGCTGAGGAGCTGAGGAGCTGAG 1860

Qy 1861 GGGAGAGAGAGACAATCGGCTGCGACTCAGAGGCTCAAAAGGAGCTTGTGCTGCTC 1920

Db 1861 GGGAGAGAGAGACAATCGGCTGCGACTCAGAGGCTCAAAAGGAGCTTGTGCTGCTC 1920

Qy 1921 ACTCATCTGCGACCCCAAGATGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980

Db 1921 ACTCATCTGCGACCCCAAGATGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980

Qy 1981 CGGACGTTTCTGTTGAAATCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040

Db 1981 CGGACGTTTCTGTTGAAATCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040

Qy 2041 GGAGTGGTGGTGAAGAGGCGGATGCTCAGCTCAGATCCAGAGGAGGAGGAGGAGGAG 2100

Db 2041 GGAGTGGTGGTGAAGAGGCGGATGCTCAGCTCAGATCCAGAGGAGGAGGAGGAGGAG 2100

Qy 2101 GGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160

Db 2101 GGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160

Qy 2161 AGCCCTCATCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220

Db 2161 AGCCCTCATCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220

Qy 2221 CACTCAGCTTGTGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2280

Db 2221 CACTCAGCTTGTGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2280

Qy 2281 CTTGACCTCGGGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340

Db 2281 CTTGACCTCGGGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340

Qy 2341 CTGCACACAGTATAGTACCAAAAGATAAAGCGCAATTAATTCAGAAAAAAA 2395

Db 2341 CTGCACACAGTATAGTACCAAAAGATAAAGCGCAATTAATTCAGAAAAAAA 2395

RESULT 7

ABL88217
ID ABL88217 standard; cDNA; 2395 BP.
XX ABL88217;
AC
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO4405 cDNA sequence SEQ ID NO:291.

Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;
vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
gene therapy; cardiovascular disorder; endothelial disorder; cancer;
angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
age-related macular degeneration; arterial restenosis; angina;
rheumatoid arthritis; myocardial infarction; thrombophlebitis;
lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
wound healing; chromosome mapping; gene mapping; gene; ss.

Homo sapiens.

WO200200690-A2.

03-JAN-2002.

20-JUN-2001; 2001WO-US019692.

23-JUN-2000; 2000US-0213637P.

20-JUL-2000; 2000US-0219556P.

25-JUL-2000; 2000US-0220624P.

28-JUL-2000; 2000US-0220664P.

25-JUL-2000; 2000WO-US020710.

02-AUG-2000; 2000US-0222695P.

17-AUG-2000; 2000US-00643657.

23-AUG-2000; 2000WO-US023522.

24-AUG-2000; 2000WO-US023328.

07-SEP-2000; 2000US-0230978P.

18-SEP-2000; 2000US-00664610.

18-SEP-2000; 2000US-00665350.

24-OCT-2000; 2000US-0242922P.

08-NOV-2000; 2000US-00709238.

08-NOV-2000; 2000WO-US030952.

10-NOV-2000; 2000WO-US030873.

01-DEC-2000; 2000WO-US032678.

20-DEC-2000; 2000US-00747259.

20-DEC-2000; 2000WO-US034956.

22-JAN-2001; 2001US-00767609.

28-FEB-2001; 2001US-00796498.

28-FEB-2001; 2001WO-US006520.

09-MAR-2001; 2001WO-US006666.

14-MAR-2001; 2001US-00802706.

22-MAR-2001; 2001US-00808689.

05-APR-2001; 2001US-00816744.

10-MAY-2001; 2001US-00828366.

10-MAY-2001; 2001US-00854208.

25-MAY-2001; 2001US-00854280.

25-MAY-2001; 2001US-00866028.

25-MAY-2001; 2001US-00866034.

30-MAY-2001; 2001WO-US017092.

30-MAY-2001; 2001US-00870574.

01-JUN-2001; 2001WO-US017443.

01-JUN-2001; 2001WO-US017800.

(GETH) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerecht ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

Query Match				Score 2395; DB 6; Length 2395;			
Best Local Similarity				100.0%; Pred. No. 0;			
Matches 2395; Conservative				0; Mismatches			
				0; Indels		0; Gaps	
Qy	1	CCTGAGCGGAAAGCGCGCTGACAGCGGAGAGGCTCCAGGTGGGGTGGTTCGCGATC	60				
Db	1	CCTGAGCGGAAAGCGCGCTGACAGCGGAGAGGCTCCAGGTGGGGTGGTTCGCGATC	60				
Qy	61	CAGCCTAGCGTGTACAGATGGCGTGGCTCGGGACTTTCGCTACCTGTTGGCTAGCG	120				
Db	61	CAGCCTAGCGTGTACAGATGGCGTGGCTCGGGACTTTCGCTACCTGTTGGCTAGCG	120				
Qy	121	ATCGAGGTCTAGGATCGCGTCTTCCTTCGGGATTTCTCCCGCTCCCGTTCGTTCC	180				
Db	121	ATCGAGGTCTAGGATCGCGTCTTCCTTCGGGATTTCTCCCGCTCCCGTTCGTTCC	180				
Qy	181	TCTGCCAGAGCGGAAACACGAGCGGAGCGCCCGAGCGCGGACCCCTCGGCTGGAGCAGT	240				
Db	181	TCTGCCAGAGCGGAAACACGAGCGGAGCGCCCGAGCGCGGACCCCTCGGCTGGAGCAGT	240				
Qy	241	TCTAACTGGACCAAGTGGCCACCACTCTCTTCAGTAAAGTGTGTTATTTCTGATAGAT	300				
Db	241	TCTAACTGGACCAAGTGGCCACCACTCTCTTCAGTAAAGTGTGTTATTTCTGATAGAT	300				
Qy	301	GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGCTGTGAAATTTATGCCCTACACAACT	360				
Db	301	GCCTTGAGAGATGATTTTGTGTTGGGTCAAAGGCTGTGAAATTTATGCCCTACACAACT	360				
Qy	361	TACCTTGTGAAAAGAGCATCTCACAGTTTGTGCTGAGCAAGCAAGCCACCTACAGTT	420				
Db	361	TACCTTGTGAAAAGAGCATCTCACAGTTTGTGCTGAGCAAGCAAGCCACCTACAGTT	420				
Qy	421	ACTATGCTCAATCAAGGATTCAGTACGCGAGCGCTTCTGCGTCTTGTGCGAGTCAATC	480				
Db	421	ACTATGCTCAATCAAGGATTCAGTACGCGAGCGCTTCTGCGTCTTGTGCGAGTCAATC	480				
Qy	481	AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGCAAGCAAGACAGCT	540				
Db	481	AGGAACCTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATAAGCAAGCAAGACAGCT	540				
Qy	541	GGAAAAAGAAATAGTCTTTTATGGAGATGAAACCTGGTTAAATTTCCCAAGCATTTT	600				
Db	541	GGAAAAAGAAATAGTCTTTTATGGAGATGAAACCTGGTTAAATTTCCCAAGCATTTT	600				
Qy	601	GTGGATATGATGGAACACCTCATTTTTCGTGTGATTAACAGAGGTGGAATAATAT	660				
Db	601	GTGGATATGATGGAACACCTCATTTTTCGTGTGATTAACAGAGGTGGAATAATAT	660				
Qy	661	GTACGAGGCAITTTGATTAAGTATTAAAGAGGAGATTTGGACATATTAATCTCCAC	720				
Db	661	GTACGAGGCAITTTGATTAAGTATTAAAGAGGAGATTTGGACATATTAATCTCCAC	720				
Qy	721	TACCTGGGCTGGACACATTTGCGGCAATTTCAAGGCCCAAGCCCTGATTTGGGCGAG	780				
Db	721	TACCTGGGCTGGACACATTTGCGGCAATTTCAAGGCCCAAGCCCTGATTTGGGCGAG	780				
Qy	781	AGCTCAGCGAGATGACAGCGTGTGATGAAGATCCACACCTCACTGCGAGTGGAGGAG	840				
Db	781	AGCTCAGCGAGATGACAGCGTGTGATGAAGATCCACACCTCACTGCGAGTGGAGGAG	840				
Qy	841	AGAGAGCGCTTTTACCAATTTGCTGTTTGTGTCACCATGTCATGCTGGAACA	900				
Db	841	AGAGAGCGCTTTTACCAATTTGCTGTTTGTGTCACCATGTCATGCTGGAACA	900				
Qy	901	GGAGGTACCGGGCTCTCCACCGAGAGTGAATACCTCTGATTTTAAATCAGTTCT	960				
Db	901	GGAGGTACCGGGCTCTCTCCACCGAGAGTGAATACCTCTGATTTTAAATCAGTTCT	960				
Qy	961	CGCTTTGAAAGGAAACCGGTGATTCGACATCAAAGCAGCTCCAAATAGACCGGATGTG	1020				
Db	961	CGCTTTGAAAGGAAACCGGTGATTCGACATCAAAGCAGCTCCAAATAGACCGGATGTG	1020				

Qy	1021	GCTCGACACCTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGAGCCTC	1080
Db	1021	GCTCGACACCTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGAGCCTC	1080
Qy	1081	CTATTCCAGTGTGGAGGAGAACCAATGAGAGACAGTGTGAGATTTTACATTTGAAT	1140
Db	1081	CTATTCCAGTGTGGAGGAGAACCAATGAGAGACAGTGTGAGATTTTACATTTGAAT	1140
Qy	1141	ACAGTGCAGCTTAGTAAACTGTGTCAAGAGAAATGTCGCTCATATGAAAAGATCCTGG	1200
Db	1141	ACAGTGCAGCTTAGTAAACTGTGTCAAGAGAAATGTCGCTCATATGAAAAGATCCTGG	1200
Qy	1201	TTTGAAGAGTTTAAATGTGCAAGAGATGCGAACTGGATCAGATCAGATCTGACTTTGGAG	1260
Db	1201	TTTGAAGAGTTTAAATGTGCAAGAGATGCGAACTGGATCAGATCAGATCTGACTTTGGAG	1260
Qy	1261	GAAAGCAATTCAGAACTCTATTCAACCTGGGCTCCAAAGTTCTCAGGAGTACCTGGAT	1320
Db	1261	GAAAGCAATTCAGAACTCTATTCAACCTGGGCTCCAAAGTTCTCAGGAGTACCTGGAT	1320
Qy	1321	GCTCTGAAGACGCTGAGTGTCTCCCTGAGTGCAAAAGTGGCCAGTCTCACCTGCTCC	1380
Db	1321	GCTCTGAAGACGCTGAGTGTCTCCCTGAGTGCAAAAGTGGCCAGTCTCACCTGCTCC	1380
Qy	1381	TGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACTGTCATCTC	1440
Db	1381	TGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACTGTCATCTC	1440
Qy	1441	CTGGTTTCTCTGCTCTTTTATTTGTTGATCTCTGTTCTTTTGGGCGCTTTCACGTCATG	1500
Db	1441	CTGGTTTCTCTGCTCTTTTATTTGTTGATCTCTGTTCTTTTGGGCGCTTTCACGTCATG	1500
Qy	1501	TGTGACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCTCTCTGTGGCTGGCGGAGCT	1560
Db	1501	TGTGACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCTCTCTGTGGCTGGCGGAGCT	1560
Qy	1561	GCCTTTGTTTACAGACCTCTGTTGAACACCTGTTGTGTCGCAAGTCTGCGAGTGCCT	1620
Db	1561	GCCTTTGTTTACAGACCTCTGTTGAACACCTGTTGTGTCGCAAGTCTGCGAGTGCCT	1620
Qy	1621	TGGACAGGGGCTCAGGAAAGGAGCGTGGAGAGCGCTTATCCAGGCTCTGGGTGCTCC	1680
Db	1621	TGGACAGGGGCTCAGGAAAGGAGCGTGGAGAGCGCTTATCCAGGCTCTGGGTGCTCC	1680
Qy	1681	GACACAGGTTCACATCTGTGCTCAGTTCAGTTCAGTCTCTGTTGTTGAAAGTGTAGT	1740
Db	1681	GACACAGGTTCACATCTGTGCTCAGTTCAGTTCAGTCTCTGTTGTTGAAAGTGTAGT	1740
Qy	1741	TCCTGGACTGTTTACCAAGTGTGTTAAAGAGCTGGCGGTCAAGAGGAAACAGCCCC	1800
Db	1741	TCCTGGACTGTTTACCAAGTGTGTTAAAGAGCTGGCGGTCAAGAGGAAACAGCCCC	1800
Qy	1801	CAGCTGAGGGGTGTGTGAATCGGACAGCTCCAGCAGAGTGTGGAGCTGCAGCTGA	1860
Db	1801	CAGCTGAGGGGTGTGTGAATCGGACAGCTCCAGCAGAGTGTGGAGCTGCAGCTGA	1860
Qy	1861	GGAGAGAGAGCAATTCGSCCTGGACACTCAGAGGCTCAAAAGAGAGCTTGGTCCGACC	1920
Db	1861	GGAGAGAGAGCAATTCGSCCTGGACACTCAGAGGCTCAAAAGAGAGCTTGGTCCGACC	1920
Qy	1921	ACTCATCTGCCACCCCAAGATGCAATCTCTGCTCATCAGGTCCAGATTTCTTCCAGG	1980
Db	1921	ACTCATCTGCCACCCCAAGATGCAATCTCTGCTCATCAGGTCCAGATTTCTTCCAGG	1980
Qy	1981	CGGACGTTTTCTGTGGAATTTAGTCTTGGCTCGGACCTTCATTCGTTAGCTGG	2040
Db	1981	CGGACGTTTTCTGTGGAATTTAGTCTTGGCTCGGACCTTCATTCGTTAGCTGG	2040
Qy	2041	GGAGTGTGTGAGGAGTGAAGAGGCGGATGTCACACTCAGATCCACAGAGGCCA	2100
Db	2041	GGAGTGTGTGAGGAGTGAAGAGGCGGATGTCACACTCAGATCCACAGAGGCCA	2100
Qy	2101	GGATCAAGGGAGCCCACTGCACTGTCAGTGGCAGAGGACTGTTGGGCCCCCACCACCTGCAC	2160

PR 20-JUL-1999; 99US-0144791P.

QY	1	1	61	61	121
QY	CTTGGAGCCGGAAGCCGGCTGCAGCAGGCGAGGCTCCAGGTGGGTTCGTTCCGCATC	60	QY	CAGCCTAGCGTGTCCACGATGCGGCTGGGCTCGGACATTTTCGTACCTTTCGGTAGCG	120
Db	CTTGGAGCCGGAAGCCGGCTGCAGCAGGCGAGGCTCCAGGTGGGTTCGTTCCGCATC	60	Db	CAGCCTAGCGTGTCCACGATGCGGCTGGGCTCGGACATTTTCGTACCTTTCGGTAGCG	120
QY			QY	ATCCAGGTGCTAGGAGATCCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTC	180

1201	TTTGAGCAGTTTAAATGTGACAGAAATTTGATGGAACTGGATCAGACTGTACTTGGAG	1260
1261	GAAAGCAATTCAGAGTCTCTATTAACCTGGGCTCCAGGTTCTCAGGAGTACCTGGAT	1320
1261	GAAAGCAATTCAGAGTCTCTATTAACCTGGGCTCCAGGTTCTCAGGAGTACCTGGAT	1320
1321	GCTCTGAAGAGCGCTGAGTCTGCTGAGTGCACAAAGTGGCCAGTCTCACCCTGCTCC	1380
1321	GCTCTGAAGAGCGCTGAGTCTGCTGAGTGCACAAAGTGGCCAGTCTCACCCTGCTCC	1380
1381	TGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGTGGAAAGTCCCACTGTCTATC	1440
1381	TGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGTGGAAAGTCCCACTGTCTATC	1440
1441	CTGGGTTTTCTCTGCTCTTTTATTTTGGTGTATCTGCTCTTTTGGGCGCTTCACTCATG	1500
1441	CTGGGTTTTCTCTGCTCTTTTATTTTGGTGTATCTGCTCTTTTGGGCGCTTCACTCATG	1500
1501	TGTCACCTCAGCTGAAAGTTCGTCTCTCTGCTGCTCTCTGCTGCTCTCTGCTGCTGCT	1560
1501	TGTCACCTCAGCTGAAAGTTCGTCTCTCTGCTGCTCTCTGCTGCTCTCTGCTGCTGCT	1560
1561	GCCTTTGCTTTTACAGACTCTGCTGTTGAAACCTGCTGCTGCTGCTGCTGCTGCTGCT	1620
1561	GCCTTTGCTTTTACAGACTCTGCTGTTGAAACCTGCTGCTGCTGCTGCTGCTGCTGCT	1620
1621	TGACAGGGGCTTCAGGAAAGGAGCTGGAGCAGCTTATCCAGGCTCTCTGGGCTGCTCC	1680
1621	TGACAGGGGCTTCAGGAAAGGAGCTGGAGCAGCTTATCCAGGCTCTCTGGGCTGCTCC	1680
1681	GACACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1740
1681	GACACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1740
1741	TCCTGCGACTGTATACCAAGTGTATTAAGAGCTGGCGGTACAGAGCAAGCAAGCCCTC	1800
1741	TCCTGCGACTGTATACCAAGTGTATTAAGAGCTGGCGGTACAGAGCAAGCAAGCCCTC	1800
1801	CAGTGAAGGGGTGTGTGAATCGGACAGCTCCAGCAGAGAGTGTGGAGCTGCAAGTGA	1860
1801	CAGTGAAGGGGTGTGTGAATCGGACAGCTCCAGCAGAGAGTGTGGAGCTGCAAGTGA	1860
1861	GGGAAGAGAGCAATCGGCTTGGACACTCAGAGAGGTCAAAAGAGAGCTTGTGCGAC	1920
1861	GGGAAGAGAGCAATCGGCTTGGACACTCAGAGAGGTCAAAAGAGAGCTTGTGCGAC	1920
1921	ACTCATCTCGCCACCCCAAGATGCTGCTCATGAGTCCAGATTTCTTTCCAGG	1980
1921	ACTCATCTCGCCACCCCAAGATGCTGCTCATGAGTCCAGATTTCTTTCCAGG	1980
1981	CGGACCTTTCTGTTGGAATTTCTAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2040
1981	CGGACCTTTCTGTTGGAATTTCTAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2040
2041	GGAGTGTGTGAGGAGTGAAGAGAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2100
2041	GGAGTGTGTGAGGAGTGAAGAGAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2100
2101	GGATCAAGGAGCCCACTGAGTGGAGAGAGCTGTTGGGCGCCCAACCCCTGAC	2160
2101	GGATCAAGGAGCCCACTGAGTGGAGAGAGCTGTTGGGCGCCCAACCCCTGAC	2160
2161	AGCCCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2220
2161	AGCCCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2220
2221	CACCTCAGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2280
2221	CACCTCAGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2280
2281	CTTGACCTCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2340
2281	CTTGACCTCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2340
121	ATCGAGGTCTAGGATCGGCTCTCTCTCGGATTTCTTCCGGCTCCCGCTTCTGTTCC	180
181	TCTGCCAGAGGGAACAGGAGCGAGCCCGCCAGCGCCGCAACCTCTCGGCTGGAGCCAGT	240
181	TCTGCCAGAGGGAACAGGAGCGAGCCCGCCAGCGCCGCAACCTCTCGGCTGGAGCCAGT	240
241	TCTAACTGACACCGCTGACACCTCTCTCTCAGTAAAGTGTATTTGTTCTGATAGAT	300
241	TCTAACTGACACCGCTGACACCTCTCTCTCAGTAAAGTGTATTTGTTCTGATAGAT	300
301	GCCTTGAGAGATGATTTGTTGTTGGTCAAAAGGTTGGAATTTATGCTTACCAACT	360
301	GCCTTGAGAGATGATTTGTTGTTGGTCAAAAGGTTGGAATTTATGCTTACCAACT	360
361	TACCTTTGGAAGAGCACTCTCAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	420
361	TACCTTTGGAAGAGCACTCTCAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	420
421	ACTATGCTCGAATCAAGCAATTTGATGACGGGAGCTTCTCTGCTGCTGCTGCTGCTGCT	480
421	ACTATGCTCGAATCAAGCAATTTGATGACGGGAGCTTCTCTGCTGCTGCTGCTGCTGCT	480
481	AGGAACCTCAATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	540
481	AGGAACCTCAATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	540
541	GGAAAAAGATGCTTTTATGAGATGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	600
541	GGAAAAAGATGCTTTTATGAGATGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	600
601	GTGAAATGATGGAACCACTCTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	660
601	GTGAAATGATGGAACCACTCTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	660
661	GTACAGGAGCTTTGGAATAAGTATTAAGAGAGAGTGGACATATTAATCTCTCAC	720
661	GTACAGGAGCTTTGGAATAAGTATTAAGAGAGAGTGGACATATTAATCTCTCAC	720
721	TACCTGGGCTGACCACTTGGCCACATTTTCAAGGCGCCCAAGAGCTGCTGCTGCTGCTGCT	780
721	TACCTGGGCTGACCACTTGGCCACATTTTCAAGGCGCCCAAGAGCTGCTGCTGCTGCTGCT	780
781	AGCTGAGCGAGATGACAGCGTGTGATGAAGATCCACCTCACTGCTGCTGCTGCTGCTGCT	840
781	AGCTGAGCGAGATGACAGCGTGTGATGAAGATCCACCTCACTGCTGCTGCTGCTGCTGCT	840
841	AGAGAGACGCTTTTACCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	900
841	AGAGAGACGCTTTTACCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	900
901	GGAGTCAAGGCGCTCTCCAGGAGGCTGAATACCTCTGATTTTAAATCACTTCT	960
901	GGAGTCAAGGCGCTCTCCAGGAGGCTGAATACCTCTGATTTTAAATCACTTCT	960
961	GGCTTTGAAAGGAAACCGGCTGATCCGACATCCAAAGCAGCTGCTGCTGCTGCTGCTGCTGCT	1020
961	GGCTTTGAAAGGAAACCGGCTGATCCGACATCCAAAGCAGCTGCTGCTGCTGCTGCTGCTGCT	1020
1021	GCTGCGACCTGCGGATAGCACTTGGCTTACCGATTCGAAAGCAGTGTAGGAGGCTC	1080
1021	GCTGCGACCTGCGGATAGCACTTGGCTTACCGATTCGAAAGCAGTGTAGGAGGCTC	1080
1081	CTATTTCCAGTGTGGAGGAGACCAATGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140
1081	CTATTTCCAGTGTGGAGGAGACCAATGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140
1141	ACAGTGCAGCTGTAGTAAACTGTTGCAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200
1141	ACAGTGCAGCTGTAGTAAACTGTTGCAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200
1201	TTTGAGCAGTTTAAATGTGACAGAAATTTGATGGAACTGGATCAGACTGTACTTGGAG	1260

Qy	2341	CTGCACACAGTATCTAGTTACCAAAAGATAAATCGGCAATAATTGAGAAAAAAA	2395
Db	2341	CTGCACACAGTATCTAGTTACCAAAAGATAAATCGGCAATAATTGAGAAAAAAA	2395
RESULT 10			
ACA66899			
ID	ACA66899	standard; cDNA; 2395 BP.	
XX	ACA66899;		
XX	23-JUN-2003	(first entry)	
XX	cDNA encoding human PRO polypeptide #59.		
XX	Human; PRO polypeptide; secreted and transmembrane protein;		
KW	anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic;		
KW	gene; ss.		
XX	Homo sapiens.		
XX	US2003036635-A1.		
PN	20-FEB-2003.		
XX	28-AUG-2002; 2002US-00230163.		
XX	25-JUL-2000; 2000US-0220638P.		
PR	01-JUN-2001; 2001WO-US017800.		
PR	29-JUN-2001; 2001WO-US021066.		
PR	09-APR-2002; 2002US-00119480.		
XX	(GETH) GENENTECH INC.		
PA	Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;		
XX	Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;		
PI	WPI; 2003-342045/32.		
DR	P-PSDB; ABU0797.		
XX	One hundred and twenty two nucleic acids encoding PRO polypeptides;		
PT	useful for the manufacture of a medicament for diagnosing or treating		
PT	tumor.		
XX	Claim 2; Fig 117; 314pp; English.		
XX	The present invention relates to the isolation of novel human PRO		
CC	polypeptides, and the polynucleotide sequences encoding them. The PRO		
CC	polypeptides are secreted and transmembrane proteins. The PRO		
CC	polypeptides and polynucleotides are useful for preparing a medicament		
CC	useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are		
CC	useful in diagnostic assays for PRO, by detecting its expression in		
CC	specific cells, tissues or serum, and for affinity purification of PRO		
CC	from recombinant cell culture or natural sources. ACA66841-ACA66962		
CC	represent cDNA sequences encoding the human PRO polypeptides of the		
CC	invention. Note: The sequence data for this patent was obtained in		
CC	electronic format directly from the USPTO web site at		
CC	seqdata.uspto.gov/psipdEntry.html		
XX	Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;		
SQ			
Query Match	100.0%;	Score 2395;	DB 7; Length 2395;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 2395;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	CCTGGAGCCGGAGCCGGCTTCAGCAGGCGCAGGCTCCAGTGGGGTCGGTTCCGCATC	60
Db	1	CCTGGAGCCGGAGCCGGCTTCAGCAGGCGCAGGCTCCAGTGGGGTCGGTTCCGCATC	60
Qy	61	CAGCCTTAGCGTGTCCACGATCGGCTCGGGACTTCGCTACCTGTTGCGTAGCG	120
Db	61	CAGCCTTAGCGTGTCCACGATCGGCTCGGGACTTCGCTACCTGTTGCGTAGCG	120

1201 TTTGAGCAGTTTAAATCTCAGAAAGATTGATGGAACTGGATCAGACTGACTGTTGAG 1260
 1201 TTTGAGCAGTTTAAATCTCAGAAAGATTGATGGAACTGGATCAGACTGACTGTTGAG 1260
 1261 GAAAAGCAATTCAGAAAGTCTTATTAACCTGGGCTCAAGGTTCTCAGGAGTACCTGGAT 1320
 1261 GAAAAGCAATTCAGAAAGTCTTATTAACCTGGGCTCAAGGTTCTCAGGAGTACCTGGAT 1320
 1321 GCTCTGAAGACGCTGAGCTTGTCCCTTGAGTGACAAAGTGGCCAGTTCTCACCCCTGCTCC 1380
 1321 GCTCTGAAGACGCTGAGCTTGTCCCTTGAGTGACAAAGTGGCCAGTTCTCACCCCTGCTCC 1380
 1381 TGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGTGGAGTCCCACTGTCTATCTC 1440
 1381 TGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGTGGAGTCCCACTGTCTATCTC 1440
 1441 CTGGGTTTCTCTGCTCTTTATTTATTTGGTGTATCTGTTCTTTCGGCGGTTCACTCATTTG 1500
 1441 CTGGGTTTCTCTGCTCTTTATTTATTTGGTGTATCTGTTCTTTCGGCGGTTCACTCATTTG 1500
 1501 TGTGCACTCAGCTGAAAGTTCGTGCTACTTCTGTGGCTCTCTGTGGCTGGCGGAGGCT 1560
 1501 TGTGCACTCAGCTGAAAGTTCGTGCTACTTCTGTGGCTCTCTGTGGCTGGCGGAGGCT 1560
 1561 GCCTTCTGTTTACCAAGTCTCTGTTGAAACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 1561 GCCTTCTGTTTACCAAGTCTCTGTTGAAACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 1621 TGGAAGGGGCTCTCAGGAAAGAGCTGGAGCAGCTTATCCAGGCTCTGCGGTGCTGCTG 1680
 1621 TGGAAGGGGCTCTCAGGAAAGAGCTGGAGCAGCTTATCCAGGCTCTGCGGTGCTGCTG 1680
 1681 GACAGAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
 1681 GACAGAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
 1741 TCCTGCGACTGTTTACCAAGTCTCTGTTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
 1741 TCCTGCGACTGTTTACCAAGTCTCTGTTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
 1801 CAGCTGAGGGGCTGTTGATTCGACAGCTCTCCAGCAGCTGTTGGAGCTGCTGCTGCTG 1860
 1801 CAGCTGAGGGGCTGTTGATTCGACAGCTCTCCAGCAGCTGTTGGAGCTGCTGCTGCTG 1860
 1861 GGAAGAGAGCAATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
 1861 GGAAGAGAGCAATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
 1921 ACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
 1921 ACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
 1981 CGGAGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
 1981 CGGAGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
 2041 GAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
 2041 GAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
 2101 GATCAAGGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
 2101 GATCAAGGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
 2161 AGCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
 2161 AGCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
 2221 CACTCAGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
 2221 CACTCAGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
 2281 CTGCACTCGGGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340

2281 CTGCACTCGGGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
 2341 CTGCACTCGGGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2395
 2341 CTGCACTCGGGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2395

RESULT 11
 ACD68651
 ID ACD68651 standard; cDNA; 2395 BP.
 XX
 AC ACD68651;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO4405 cDNA.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytostatic;
 KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
 KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
 KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; bone disorder; cartilage disorder; sports injury;
 KW arthritis; wound; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003045687-A1.
 XX
 PD 06-MAR-2003.
 XX
 PF 12-AUG-2002; 2002US-00218631.
 XX
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 DR WPI; 2003-512315/48.
 DR P-PSDB; ABO33763.
 XX
 XX New genes, and its encoded secreted and transmembrane polypeptides, or
 PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
 PT pericyte proliferation, especially for treating lung tumors, arthritis or
 PT wounds in a mammal.
 XX
 PS Claim 2; Fig 117; 314pp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule comprising a
 CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
 CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
 CC fully defined in the specification; or (b) any of 122 nucleotide
 CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
 CC specification; or the full length coding sequence of any of these 122
 CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
 CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
 CC particularly useful for detecting tumours (e.g. lung tumour, colon
 CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour),
 CC in a mammal, for stimulating the release of TNF-alpha from human blood,
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells, for stimulating fibroblast proliferation. The PRO nucleic acid or
 CC polypeptide is also useful for treating tumours or various bone and/or
 CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
 CC PRO polypeptides are useful in drug screening, particularly as targets
 CC for therapeutic intervention in these diseases, and in the diagnostic
 CC determination of the presence of these diseases. The PRO polypeptides are
 CC also useful as molecular weight markers, or for chromosome

Qy	961	GC	GT	TT	CA	AA	G	A	A	G	A	A	C	C	G	G	T	G	A	T	C	G	A	C	A	T	C	C	A	A	A	G	A	C	G	T	C	C	A	A	T	A	G	A	C	G	A	T	G	T	G		1021
Db	961	GC	GT	TT	CA	AA	G	A	A	G	A	A	C	C	G	G	T	G	A	T	C	G	A	C	A	T	C	C	A	A	A	G	A	C	G	T	C	C	A	A	T	A	G	A	C	G	A	T	G		1020		
Qy	1021	G	C	T	C	G	C	A	C	A	T	G	G	C	G	A	T	A	G	C	A	T	T	C	C	A	A	A	G	A	C	A	G	T	G	G	A	G	A	C	A	G	T	G	A	G	A	G	C	T	C		1080
Db	1021	G	C	T	C	G	C	A	C	A	T	G	G	C	G	A	T	A	G	C	A	T	T	C	C	A	A	A	G	A	C	A	G	T	G	G	A	G	A	C	A	G	T	G	A	G	A	G	C	T	C		1080
Qy	1081	C	T	A	T	C	C	C	A	G	T	T	G	G	A	G	A	C	C	A	A	T	G	A	G	A	G	A	C	A	G	A	G	A	G	A	G	A	C	A	G	A	G	A	G	A	T	T	T		1140		
Db	1081	C	T	A	T	C	C	C	A	G	T	T	G	G	A	G	A	C	C	A	A	T	G	A	G	A	G	A	C	A	G	A	G	A	G	A	G	A	C	A	G	A	G	A	G	A	T	T	T		1140		
Qy	1141	A	C	A	G	T	C	A	G	C	T	T	A	A	C	T	T	G	C	A	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		1200				
Db	1141	A	C	A	G	T	C	A	G	C	T	T	A	A	C	T	T	G	C	A	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		1200					
Qy	1201	T	T	T	G	A	G	C	A	G	T	T	A	A	A	T	T	G	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		1260					
Db	1201	T	T	T	G	A	G	C	A	G	T	T	A	A	A	T	T	G	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		1260					
Qy	1261	G	A	A	A	G	A	C	T	C	A	G	A	A	G	T	C	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		1320					
Db	1261	G	A	A	A	G	A	C	T	C	A	G	A	A	G	T	C	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		1320					
Qy	1321	G	C	T	C	T	A	A	G	A	G	C	T	G	A	G	T	T	G	C	C	T	C	A	G	A	G	T	C	C	A	G	A	G	T	C	C	A	G	A	G	T	C	C	A	G	T		1380				
Db	1321	G	C	T	C	T	A	A	G	A	G	C	T	G	A	G	T	T	G	C	C	T	C	A	G	A	G	T	C	C	A	G	A	G	T	C	C	A	G	A	G	T	C	C	A	G	T		1380				
Qy	1381	T	G	C	T	C	A	G	C	T	C	C	A	A	G	A	A	G	T	C	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		1440					
Db	1381	T	G	C	T	C	A	G	C	T	C	C	A	A	G																																						

RESULT 13
ACD81610

ID ACD81610 standard; cDNA; 2395 BP.

AA ACD81610;

XX

DT 18-SEP-2003 (first entry)

XX

DE Human cDNA encoding secreted/transmembrane protein PRO4405.

XX Human; ss; gene; secreted/transmembrane protein; PRO; tumour; cancer;
KW cytostatic.

OS Homo sapiens.

PN US2003009013-A1.

PD 09-JAN-2003.

PF 01-MAY-2002; 2002US-00063519.

PR 30-DEC-1998; 98KR-00062142.

PR 08-MAR-1999; 99WO-US005028.
PR 08-MAR-1999; 99WO-US005028.

PR 14-MAY-1999; 99US-00311832.

PR 14-MAY-1999; 99WO-US010733.

PR 25-AUG-1999; 99US-00380137.

PR 25-AUG-1999; 99US-00380138.

PR 25-AUG-1999; 99US-00380139.

PR 25-AUG-1999; 99US-00380142.

PR 15-SEP-1999; 99US-00397342.

PR 18-OCT-1999; 99US-00403297.

PR 12-NOV-1999; 99US-00423844.

PR 30-DEC-1999; 99WO-US031274.
 PR 10 FEB 2000 000000Z
 PR 10 FEB 2000 000000Z

PR I8-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005531
PR 01-MAR-2000; 2000WO-US005531

PR 01-MAR-2000; 2000WD-US005601.
PR 02-MAR-2000; 2000WD-US005601.
PR 03-MAR-2000; 2000WD-US005601.

02-MAR-2000; 2000WC-US005841.
21-MAR-2000; 2000WC-US007533

21-MAR-2000; 2000WO-US007532.
22-MAY-2000: 2000WO-IIS014042

PR 02-JUN-2000: 2000WO-IIS015264

22-AUG-2000: 2000US-00644848

24-AUG-2000: 2000WO-US023328 PR

18-SEP-2000: 2000US-00664610
PR

PR 18-SEP-2000; 2000US-00665350.

PR 08-NOV-2000; 2000US-00709238.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX (GETH) GENENTECH INC.
PA
XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-447384/42.
DR P-PSDB; ABO34004.
XX New isolated antibody specifically binding a PRO polypeptide, useful for
PT the preparation of a medicament for treating disorders with the aberrant
PT expression or activity of the PRO polypeptide, such as tumor conditions
PT and cancer.
XX Disclosure; Fig 139; 223pp; English.
XX The invention relates to an antibody that binds to a secreted or
CC transmembrane protein designated PRO1446 appearing as ABO33941. The
CC protein is one of 84 PRO polypeptides which (along with their encoding
CC nucleic acids) are disclosed in the specification. The methods and
CC compositions of the present invention are useful for the preparation of a
CC medicament for the treatment of disorders associated with the aberrant
CC expression or activity of the PRO polypeptide, such as tumour conditions
CC and cancer. They can also be used to generate transgenic or knockout
CC animals useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The antibodies may be used in various
CC diagnostic, competitive binding and/or immunoprecipitation assays. The
CC present sequence encodes a PRO polypeptide
XX Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 2395; DB 7; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGAGCGGAGCGGGCTGCGAGCGGCGAGGCTCCAGGTGGGGTTCGGTTCGGCATC 60
DB 1 CCTGGAGCGGAGCGGGCTGCGAGCGGCGAGGCTCCAGGTGGGGTTCGGTTCGGCATC 60
QY 61 CAGCTAGCGGTGTCACGATCGGCTGGGCTCCGGGACTTCGCTACTGTTGGTAGCG 120
DB 61 CAGCTAGCGGTGTCACGATCGGCTGGGCTCCGGGACTTCGCTACTGTTGGTAGCG 120
QY 121 ATCAGGTGCTAGGATCGGCTTCCTTCGGGATTCCTCCGGCTCCCGTTCGTTCC 180
DB 121 ATCAGGTGCTAGGATCGGCTTCCTTCGGGATTCCTCCGGCTCCCGTTCGTTCC 180
QY 181 TCTGCCAGCGGAGACACGAGCGGAGCCCGCCAGCGCCCGAACCTCGGCTGGAGCCAGT 240
DB 181 TCTGCCAGCGGAGACACGAGCGGAGCCCGCCAGCGCCCGAACCTCGGCTGGAGCCAGT 240
QY 241 TCTAACTGGACACCGCTGCCACCTCTCTTCAGTAAAGTGTGTTGTTCTGATAGAT 300
DB 241 TCTAACTGGACACCGCTGCCACCTCTCTTCAGTAAAGTGTGTTGTTCTGATAGAT 300
QY 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAAGGTGTGAATTTATGCCCTACCAACT 360
DB 301 GCCTTGAGAGATGATTTTGTGTTGGGTCAAAAGGTGTGAATTTATGCCCTACCAACT 360
QY 361 TACCTTGTGGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT 420
DB 361 TACCTTGTGGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT 420
Db 361 TACCTTGTGGAAAAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAGCCACCTACAGTT 420
QY 421 ACTATGCCCTCGAATCAAGGCAATTTGATGACGGGAGACCTTCTGGCTTTGTGTCAGCTCATC 480
Db 421 ACTATGCCCTCGAATCAAGGCAATTTGATGACGGGAGACCTTCTGGCTTTGTGTCAGCTCATC 480
QY 481 AGGAACTCTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 AGGAACTCTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 GGAAGAAAGATAGTCTTTTATGAGATGAAACCTGGGTTTAAATTTATTTCCAAAGCATTTT 600
Db 541 GGAAGAAAGATAGTCTTTTATGAGATGAAACCTGGGTTTAAATTTATTTCCAAAGCATTTT 600
QY 601 GTGGAATATGATGGAACCAACCTCATTTTTCGTGTAGATATACACAGAGGTGATATATAT 660
Db 601 GTGGAATATGATGGAACCAACCTCATTTTTCGTGTAGATATACACAGAGGTGATATATAT 660
QY 661 GTCACAGGCAATTTGGATTAAGTATTTAAAGAGGAGATTTGGGACATATTAATCCTCCAC 720
Db 661 GTCACAGGCAATTTGGATTAAGTATTTAAAGAGGAGATTTGGGACATATTAATCCTCCAC 720
QY 721 TACCTGGGCTGGACCAATTTGCCACATTTTCAAGGCCCAACAGCCCCCTGATTGGGCGAG 780
Db 721 TACCTGGGCTGGACCAATTTGCCACATTTTCAAGGCCCAACAGCCCCCTGATTGGGCGAG 780
QY 781 AAGCTGAGCGAGATGAGACGCTGCTGATGAAGATCCACACCTCATCTGAGTGAAGGAG 840
Db 781 AAGCTGAGCGAGATGAGACGCTGCTGATGAAGATCCACACCTCATCTGAGTGAAGGAG 840
QY 841 AGAGAGAGCGCTTTACCCAAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 841 AGAGAGAGCGCTTTTACCCAAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 GGAAGTCAAGCGGCTCTCTCCAGGAGGAGTGAATACACCTCTGATTTTAAATCAGTTCT 960
Db 901 GGAAGTCAAGCGGCTCTCTCCAGGAGGAGTGAATACACCTCTGATTTTAAATCAGTTCT 960
QY 961 GCGTTTGAAGAGAAACCCGGTGATATCCGACATCCAAAGCACGCTCCAAATGAGCGATGTG 1020
Db 961 GCGTTTGAAGAGAAACCCGGTGATATCCGACATCCAAAGCACGCTCCAAATGAGCGATGTG 1020
QY 1021 GCTGCGACATGCGGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGAGGCTC 1080
Db 1021 GCTGCGACATGCGGATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGAGGCTC 1080
QY 1081 CTATTTCCAGTTTGGAGAGGAGACCAATGAGAGAGAGTGTGAGATTTTACATTTGAAT 1140
Db 1081 CTATTTCCAGTTTGGAGAGGAGACCAATGAGAGAGAGTGTGAGATTTTACATTTGAAT 1140
QY 1141 ACAGTGCAGCTTGTAAACCTGTTGCAAGAGATGTGCGCTCATATGAAGAAAGTCTCTGG 1200
Db 1141 ACAGTGCAGCTTGTAAACCTGTTGCAAGAGATGTGCGCTCATATGAAGAAAGTCTCTGG 1200
QY 1201 TTTGAGCAGTTTAAATGCTCAGAAAGATGTCATGGAACCTGATCAGACTGTACTTGGAG 1260
Db 1201 TTTGAGCAGTTTAAATGCTCAGAAAGATGTCATGGAACCTGATCAGACTGTACTTGGAG 1260
QY 1261 GAAAGCAATTCAGAAAGTCTTATTCAACTGGGCTCCAAAGGTTTCTCAGGAGTACTGTGAT 1320
Db 1261 GAAAGCAATTCAGAAAGTCTTATTCAACTGGGCTCCAAAGGTTTCTCAGGAGTACTGTGAT 1320
QY 1321 GCTCTGAAGAGCGCTGAGCTTGTCCCTGAGTGCACAGTGGCCAGTCTTCACTCCCTGCTCC 1380
Db 1321 GCTCTGAAGAGCGCTGAGCTTGTCCCTGAGTGCACAGTGGCCAGTCTTCACTCCCTGCTCC 1380
QY 1381 TGCTCAGGCTCCACAGGCACTGTCACAGAGGCTGAGCTGGAAGTCCCACTGTCTATCTC 1440
Db 1381 TGCTCAGGCTCCACAGGCACTGTCACAGAGGCTGAGCTGGAAGTCCCACTGTCTATCTC 1440
QY 1441 CTGGGTTTCTGCTCTTTTATTTGTTGATCTCTGGTCTTTTGGGCGGTTTACGTCATTG 1500
Db 1441 CTGGGTTTCTGCTCTTTTATTTGTTGATCTCTGGTCTTTTGGGCGGTTTACGTCATTG 1500

PT	as diabetes, obesity and/or hypoinsulinemia.	
XX	Claim 1; Fig 19; 196pp; English.	
PS	The invention relates to a new isolated nucleic acid which encodes a PRO	
XX	polypeptide. The methods and compositions of the present invention are	
CC	useful for the diagnosis and treatment of disorders associated with the	
CC	PRO polypeptides, such as diabetes, obesity and hypoinsulinemia. The	
CC	present sequence represents cDNA encoding a human secreted and	
CC	transmembrane PRO polypeptide	
XX	Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;	
SQ	Query Match 100.0%; Score 2395; DB 7; Length 2395;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CCTGGAGCGGAAGCGCGCTGCAGCAGGCGGAGGCTCCAGGTGGGGTCGGTCATC 60	
DB	1 CCTGGAGCGGAAGCGCGCTGCAGCAGGCGGAGGCTCCAGGTGGGGTCGGTCATC 60	
QY	61 CAGCCTAGCGTGTCCAGATGCGGCTGGGCTCCGGGACTTTCGTACCTGTTGGTAGCG 120	
DB	61 CAGCCTAGCGTGTCCAGATGCGGCTGGGCTCCGGGACTTTCGTACCTGTTGGTAGCG 120	
QY	121 ATCAGAGTGTAGGATCGCGGTCTTCTTCCTCGGGATTCTCCCGGCTCCCGTTGTTCC 180	
DB	121 ATCAGAGTGTAGGATCGCGGTCTTCTTCCTCGGGATTCTCCCGGCTCCCGTTGTTCC 180	
QY	181 TCTGCCAGAGCGGAACACAGCAGGCGGAGCCCGCCAGCGCCGAAACCTCGGCTGGAGCCAGT 240	
DB	181 TCTGCCAGAGCGGAACACAGCAGGCGGAGCCCGCCAGCGCCGAAACCTCGGCTGGAGCCAGT 240	
QY	241 TCTAACTGGACCGCTGCCACCACTCTCTTCAGTAAAGTGTATTTGTTCTGATAGAT 300	
DB	241 TCTAACTGGACCGCTGCCACCACTCTCTTCAGTAAAGTGTATTTGTTCTGATAGAT 300	
QY	301 GCCTTGAGAGATGATTTGTTGGTCAAGGGTGTGAATTTATGTCCTACACAACT 360	
DB	301 GCCTTGAGAGATGATTTGTTGGTCAAGGGTGTGAATTTATGTCCTACACAACT 360	
QY	361 TACCTTGTGGAAGAGAGATCTCACAGTTTTCGTGGCTGAAGCAAGCCACCTACAGTT 420	
DB	361 TACCTTGTGGAAGAGAGATCTCACAGTTTTCGTGGCTGAAGCAAGCCACCTACAGTT 420	
QY	421 ACTATGCTCGAATCAAGGCAATGATGACGGGAGCCCTTCCTGGCTTGTGCGATC 480	
DB	421 ACTATGCTCGAATCAAGGCAATGATGACGGGAGCCCTTCCTGGCTTGTGCGATC 480	
QY	481 AGGAACCTCAATTCCTGCACTGTGGAACACAGTGTGATAAGACAAAGCAAGCAGCT 540	
DB	481 AGGAACCTCAATTCCTGCACTGTGGAACACAGTGTGATAAGACAAAGCAAGCAGCT 540	
QY	541 GGAAGAAAGATGCTTTTATGGAGATGAACCTGGGTTAAATTTATCCCAAGCATTTT 600	
DB	541 GGAAGAAAGATGCTTTTATGGAGATGAACCTGGGTTAAATTTATCCCAAGCATTTT 600	
QY	601 GTGGAATATGATGAAACCACTTTTCTGTCAGATTACACAGAGTGGATAATAT 660	
DB	601 GTGGAATATGATGAAACCACTTTTCTGTCAGATTACACAGAGTGGATAATAT 660	
QY	661 GTCCAGGCAATTTGGATAAAGTATTAAGAGAGAGATTTGGACATATTAATCTCCAC 720	
DB	661 GTCCAGGCAATTTGGATAAAGTATTAAGAGAGAGATTTGGACATATTAATCTCCAC 720	
QY	721 TACCTGGGGCTGGACCAATTGGCCACATTTTACAGGCCCAACAGCCCTGATGGGAG 780	
DB	721 TACCTGGGGCTGGACCAATTGGCCACATTTTACAGGCCCAACAGCCCTGATGGGAG 780	
QY	781 AAGCTGAGCGAGATGGAAGCGTGTGATGAGATCCACCTCACTGAGTCGAGGAG 840	
DB	781 AAGCTGAGCGAGATGGAAGCGTGTGATGAGATCCACCTCACTGAGTCGAGGAG 840	

QY	841 AGAGAGAGCCCTTTACCCAAATTTGCTGTTCTTTGTTGACCATGGCATGCTGAAACA 900	
DB	841 AGAGAGAGCCCTTTACCCAAATTTGCTGTTCTTTGTTGACCATGGCATGCTGAAACA 900	
QY	901 GGAAGTCACGGGGCTCTCCACCGAGGAGTGAATACACCTCTGATTTTAAATCAGTTCT 960	
DB	901 GGAAGTCACGGGGCTCTCCACCGAGGAGTGAATACACCTCTGATTTTAAATCAGTTCT 960	
QY	961 GCGTTTGAAGGAAACCCCGGTGATATCCGACATCCAAAGCACGTCCTCAATAGACGATG 1020	
DB	961 GCGTTTGAAGGAAACCCCGGTGATATCCGACATCCAAAGCACGTCCTCAATAGACGATG 1020	
QY	1021 GCTGCACACTGGCGATAGACCTTGCTGCTACCGATTCGAAACACAGTGTAGGAGCCTC 1080	
DB	1021 GCTGCACACTGGCGATAGACCTTGCTGCTACCGATTCGAAACACAGTGTAGGAGCCTC 1080	
QY	1081 CTATTTCCAGTTGTGGAAGGAGACCAATGAGAGACAGTTGAGATTTTACATTTGAAT 1140	
DB	1081 CTATTTCCAGTTGTGGAAGGAGACCAATGAGAGACAGTTGAGATTTTACATTTGAAT 1140	
QY	1141 ACAGTCAGCTTAAATCTGTTTGAAGAGAAATGTGCGCTCATATGAAAAGATTCCTGG 1200	
DB	1141 ACAGTCAGCTTAAATCTGTTTGAAGAGAAATGTGCGCTCATATGAAAAGATTCCTGG 1200	
QY	1201 TTTGAGCAGTTTAAATGTGCAAGAGATTTGCATGGGACCTGGATCAGACTGTACTTGAG 1260	
DB	1201 TTTGAGCAGTTTAAATGTGCAAGAGATTTGCATGGGACCTGGATCAGACTGTACTTGAG 1260	
QY	1261 GAAAGCATTCAGAGTCTTATTAACCTGGGCTCCAAAGGTTCTCAGGACAGTACCTGGAT 1320	
DB	1261 GAAAGCATTCAGAGTCTTATTAACCTGGGCTCCAAAGGTTCTCAGGACAGTACCTGGAT 1320	
QY	1321 GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCAAAAGTGGCCAGTTCACCTGCTCC 1380	
DB	1321 GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCAAAAGTGGCCAGTTCACCTGCTCC 1380	
QY	1381 TGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCAGTGCATCTC 1440	
DB	1381 TGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCAGTGCATCTC 1440	
QY	1441 CTGGGTTTCTCTGCTCTTTTATTTGTTGATTCCTGGTTCCTTCGGCCGTTTCACTCA 1500	
DB	1441 CTGGGTTTCTCTGCTCTTTTATTTGTTGATTCCTGGTTCCTTCGGCCGTTTCACTCA 1500	
QY	1501 TGTGCACTCAGCTGAAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560	
DB	1501 TGTGCACTCAGCTGAAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560	
QY	1561 GCCTTTGCTTTTACAGACTCTGGTTGAAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620	
DB	1561 GCCTTTGCTTTTACAGACTCTGGTTGAAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620	
QY	1621 TGGAACAGGGGCTCAGGGAAGGAGCTGGAGCAGCTTATCCAGGCTCTGCTGCTGCTG 1680	
DB	1621 TGGAACAGGGGCTCAGGGAAGGAGCTGGAGCAGCTTATCCAGGCTCTGCTGCTGCTG 1680	
QY	1681 GACAAGGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740	
DB	1681 GACAAGGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740	
QY	1741 TCCTGCGACTGTTTACCAAGGTTGTTAAAGAGCTGGCGGTTCACAGAGCAACAGCC 1800	
DB	1741 TCCTGCGACTGTTTACCAAGGTTGTTAAAGAGCTGGCGGTTCACAGAGCAACAGCC 1800	
QY	1801 CAGCTGAGGGGCTGTGTAATCGGACAGCTCCAGCAGAGTGTGGAGCTGCGAGCTGA 1860	
DB	1801 CAGCTGAGGGGCTGTGTAATCGGACAGCTCCAGCAGAGTGTGGAGCTGCGAGCTGA 1860	
QY	1861 GGGAGAGAGAGCAATTCGGCTTGGACCTCAGGAGGCTCAAGAGAGACTTCTGCTGAC 1920	
DB	1861 GGGAGAGAGAGCAATTCGGCTTGGACCTCAGGAGGCTCAAGAGAGACTTCTGCTGAC 1920	
QY	1921 ACTCATCTCTGCCACCCCGAGAAATGATCTCTGCTCATCAGGTCAGATTTCTTTCC 1980	
DB	1921 ACTCATCTCTGCCACCCCGAGAAATGATCTCTGCTCATCAGGTCAGATTTCTTTCC 1980	

Db 1921 ACTCATCTGCGCCACCCCGAATGCACTCTGCTCATAGTCCAGATTCTTTCACAGG 1980
QY 1981 CGGACGTTTTCTGTGGAAATCTTACTCTTGGCTCGGACACCTTCATTGTTAGCTGG 2040
Db 1981 CGGACGTTTTCTGTGGAAATCTTACTCTTGGCTCGGACACCTTCATTGTTAGCTGG 2040
QY 2041 GGAGTGGTGGTAGGAGTGAAGAAGAGGCGGATGTCACACTCAGATCCACAGAGCCCA 2100
Db 2041 GGAGTGGTGGTAGGAGTGAAGAAGAGGCGGATGTCACACTCAGATCCACAGAGCCCA 2100
QY 2101 GGATCAAGGAGCCCACTCGAGTGGCAGGAGGAGTGTGGGCCCCCACCCTTGGAC 2160
Db 2101 GGATCAAGGAGCCCACTCGAGTGGCAGGAGGAGTGTGGGCCCCCACCCTTGGAC 2160
QY 2161 AGCCCTCATCCCTCTTGGCTTGAGCGCTGAGAGGCCCTGTGTGAGTGTCTGACCGAGA 2220
Db 2161 AGCCCTCATCCCTCTTGGCTTGAGCGCTGAGAGGCCCTGTGTGAGTGTCTGACCGAGA 2220
QY 2221 CACTCAGCTTTGTTCATCAGGSCACAGGCTTCTCGAGCCAGGATGATCTGTGCCAG 2280
Db 2221 CACTCAGCTTTGTTCATCAGGSCACAGGCTTCTCGAGCCAGGATGATCTGTGCCAG 2280
QY 2281 CTGTGACCTCGGSCCATCTGGGCTCATGCTCTCTCTCTGCTTATTTAGTACTAG 2340
Db 2281 CTGTGACCTCGGSCCATCTGGGCTCATGCTCTCTCTCTGCTTATTTAGTACTAG 2340
QY 2341 CTGCAACAGTATGTAGTTACCAAAAGAAATAACGGCAATATTGAGAAAAAAA 2395
Db 2341 CTGCAACAGTATGTAGTTACCAAAAGAAATAACGGCAATATTGAGAAAAAAA 2395

RESULT 15
ACA60432

ID ACA60432 standard; cDNA; 2395 BP.

AC ACA60432;

DT 11-JUN-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO4405 cDNA.

KW Human; secreted and transmembrane polypeptide; gene;

KW ss. chromosome mapping; gene mapping; transgenic animal; knockout animal;
KW therapeutic agent screening; chromosome identification; tissue typing;
KW gene therapy.

OS Homo sapiens.

PN US2003018183-A1.

XX 23-JAN-2003.

PF 01-MAY-2002; 2002US-00063512.

PR 06-DEC-2001; 2001US-00006867.

PA (GETH) GENENTECH INC.

PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

DR WPI; 2003-330984/31.

DR P-PSDB; ABU72021.

XX New secreted and transmembrane PRO polypeptides and nucleic acid
PT molecules encoding the polypeptides, useful in gene therapy or preparing
PT a medicament for treating a condition that is responsive to the PRO
PT polypeptide or antibody.

XX Disclosure; Fig 139; 409pp; English.

XX The invention describes novel isolated PRO polypeptides. The PRO

CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide

SQ Sequence 2395 BP; 566 A; 605 C; 656 G; 568 T; 0 U; 0 Other;

Query Match 100.0%; Score 2395; DB 7; Length 2395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGAGCCGGAAGCGCGGCTGCAGCAGGCGGAGGCTCCAGGTGGGTGGTTCGCGATC 60

Db 1 CCTGGAGCCGGAAGCGCGGCTGCAGCAGGCGGAGGCTCCAGGTGGGTGGTTCGCGATC 60

QY 61 CAGCCTTAGCTGTCCACAGATGGGCTCGGACCTTTCGGGACTTTCGCTACCTGTTCCGTAGCG 120

Db 61 CAGCCTTAGCTGTCCACAGATGGGCTCGGACCTTTCGGGACTTTCGCTACCTGTTCCGTAGCG 120

QY 121 ATCGAGGTCTAGGAGTCCGGTCTTCCTTCGGGGGATTTCCCGGCTCCCGTTCGTTCC 180

Db 121 ATCGAGGTCTAGGAGTCCGGTCTTCCTTCGGGGGATTTCCCGGCTCCCGTTCGTTCC 180

QY 181 TCTGCCAGAGCGGAACACGAGGCGGAGCCGCCAGCGCCCGAACCTTCGCTGGAGCCAGT 240

Db 181 TCTGCCAGAGCGGAACACGAGGCGGAGCCGCCAGCGCCCGAACCTTCGCTGGAGCCAGT 240

QY 241 TCTAAGTGGACCAAGCTGCGCACCTCTCTTCAGTAAAGTTGTTATTTCTGTAGAT 300

Db 241 TCTAAGTGGACCAAGCTGCGCACCTCTCTTCAGTAAAGTTGTTATTTCTGTAGAT 300

QY 301 GCCTTGAGAGATGATTTGTGTTGGGTCAAGGGTGTGAATTTATGCGCTTACAACT 360

Db 301 GCCTTGAGAGATGATTTGTGTTGGGTCAAGGGTGTGAATTTATGCGCTTACAACT 360

QY 361 TACCTTGTGAAAAAGGAGCATCTCACAGTCTTGTGGCTGAAGCAAGCCACCTACAGTT 420

Db 361 TACCTTGTGAAAAAGGAGCATCTCACAGTCTTGTGGCTGAAGCAAGCCACCTACAGTT 420

QY 421 ACTATGCTTGAATCAAGGCATTGATGCGGGAGCCTTCTCGGCTTTCGACGTCATC 480

Db 421 ACTATGCTTGAATCAAGGCATTGATGCGGGAGCCTTCTCGGCTTTCGACGTCATC 480

QY 481 AGGAACCTCAATTTCTCTGCACTGTGGAAGAGCATCTCACAGTCTTGTGGCTGAAGCAAGCCACCTACAGTT 540

Db 481 AGGAACCTCAATTTCTCTGCACTGTGGAAGAGCATCTCACAGTCTTGTGGCTGAAGCAAGCCACCTACAGTT 540

QY 541 GAAAAAAGAAATAGTCTTTTATCGAGATGAACCTCGGTTAAATTTATCCCAAGCATTTT 600

Db 541 GAAAAAAGAAATAGTCTTTTATCGAGATGAACCTCGGTTAAATTTATCCCAAGCATTTT 600

QY 601 GTGGAATATGATGGAACCAACCTCATTTTTCGTTGTCAGATTACACAGAGTGGATAATAT 660

Db 601 GTGGAATATGATGGAACCAACCTCATTTTTCGTTGTCAGATTACACAGAGTGGATAATAT 660

QY 661 GTACAGAGCATTTGGATAAAGTATTAAGAGAGAGATTGGGACATATTATTCCTCCAC 720

Db 661 GTACAGAGCATTTGGATAAAGTATTAAGAGAGAGATTGGGACATATTATTCCTCCAC 720

QY 721 TACCTGGGGCTGGACCAATTTGCGCACATTTTCAGGCGCCCAACAGCCCTGATTCGGGAG 780

Db 721 TACCTGGGGCTGGACCAATTTGCGCACATTTTCAGGCGCCCAACAGCCCTGATTCGGGAG 780

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2004, 08:51:20 ; Search time 58 Seconds
(without alignments)
3.894 Million cell updates/sec

Title: US-10-036-150-44
Perfect score: 2395
Sequence: 1 cctggagccgaagcgccg.....gcaataattgagaaaaaaa 2395

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 60 segs, 47150 residues

Total number of hits satisfying chosen parameters: 120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : rst44.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	405	16.9	418	1	ACCESSION: AQ673215
2	395.2	16.5	434	1	ACCESSION: BE549374
C 3	390.4	16.3	1201	1	ACCESSION: BX377107
C 4	371.8	15.5	390	1	ACCESSION: BX097186
5	371.8	15.5	640	1	ACCESSION: BU425116
6	356.7	14.9	920	1	ACCESSION: BG336024
7	356.7	14.9	970	1	ACCESSION: BG336399
8	340.5	14.2	674	1	ACCESSION: BG927822
9	338	14.1	557	1	ACCESSION: BE757899
C 10	314.2	13.1	368	1	ACCESSION: AW262524
11	309.7	12.9	332	1	ACCESSION: BM844459
C 12	308.9	12.9	535	1	ACCESSION: BG346870
C 13	305.6	12.8	405	1	ACCESSION: AW262485
14	304	12.7	570	1	ACCESSION: BE669243
C 15	300.799	12.6	739	1	ACCESSION: CA377408
16	300.6	12.6	319	1	ACCESSION: AA687924
C 17	295.6	12.3	412	1	ACCESSION: BM107678
18	287.8	12.0	753	1	ACCESSION: BM107678
19	287.2	12.0	508	1	ACCESSION: BI919095
20	281.3	11.7	631	1	ACCESSION: CB783017
C 21	263	11.0	510	1	ACCESSION: AL871903
22	248.4	10.4	418	1	ACCESSION: CB548333
C 23	237.9	9.9	253	1	ACCESSION: CB765650
24	229	9.6	976	1	ACCESSION: AA361388
25	217.4	9.1	233	1	ACCESSION: CD516167
26	211	8.8	1205	1	ACCESSION: CD516167
C 27	206.2	8.6	350	1	ACCESSION: BF791461
28	205	8.6	318	1	ACCESSION: BQ293001
C 29	200	8.4	806	1	ACCESSION: Z44206
30	200	8.4	3150	1	ACCESSION: BG923173
31	199	8.3	1099	1	ACCESSION: BC051059
32	192.4	8.0	789	1	ACCESSION: BM455257
33	191.7	8.0	501	1	ACCESSION: BG389289
					ACCESSION: CG592530

C 34	184.5	7.7	318	1	BI051441
35	173.6	7.2	517	1	BI391754
C 36	172.6	7.2	355	1	BF746141
C 37	165.2	6.9	264	1	BI026475
38	163.4	6.8	764	1	EX077539
C 39	160.4	6.7	252	1	AA356939
C 40	158.2	6.6	744	1	EX077538
41	153.8	6.4	739	1	BI030677
42	123	5.1	758	1	BI080925
C 43	116.4	4.9	460	1	BF42617
44	114.6	4.8	510	1	AL913388
45	110.4	4.6	720	1	CE024824
C 46	108.4	4.5	934	1	BE897861
47	107.4	4.5	122	1	BQ360060
C 48	106.8	4.5	556	1	BM323673
49	106.8	4.5	651	1	BQ522572
C 50	103.1	4.3	990	1	BM468049
51	103.1	4.3	2495	1	BC036916
C 52	103.1	4.3	3270	1	AY408630
53	102.5	4.3	466	1	BZ270849
C 54	99.4001	4.2	560	1	BJ434815
55	96.6002	4.0	880	1	CD387014
C 56	96.2002	4.0	3270	1	AY408631
57	93.8002	3.9	545	1	AW862654
C 58	90.6002	3.8	3282	1	AY408632
59	89	3.7	124	1	BE685541
C 60	87.8	3.7	140	1	CD733602

ALIGNMENTS

RESULT 1
LOCUS AQ673215/c 418 bp DNA linear GSS 24-JUN-1999
DEFINITION HS_5496_A2_G07_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1072 Col=14 Row=M, genomic survey sequence.
ACCESSION AQ673215 GI:5205961
VERSION AQ673215.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 418)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1072 row: M column: 14
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 418.
Location/Qualifiers
1..418
/organism="Homo sapiens"

FEATURES
source

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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="IMAGE:3460537"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/notes="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

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Query Match      16.9%; Score 405; DB 1; Length 418;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 408; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1589 CACCTGGTGTGTCACCAAGTGTGGCAGTGCCTCCGACAGGGGGCCCTCAGGGAAGACGTG 1648
DB 418 CACATGGTGTGTCACCAAGTGTGGCAGTGCCTCCGACAGGGGGCCCTCAGGGAAGACGTG 359

QY 1649 GAGCAGCCTTATCCAGGCTTGGGTGTCGCGACACAGAGTGTTCACATCTGTGCTGTCA 1708
DB 358 GAGCAGCCTTATCCAGGCTTGGGTGTCGCGACACAGAGTGTTCACATCTGTGCTGTCA 299

QY 1709 GGTGAGTGCCTCAGTCTTGTGAAAGCTAGTGTTCCTGCGACTGTACCAAGCTGATTGTA 1768
DB 298 GGTGAGTGCCTCAGTCTTGTGAAAGCTAGTGTTCCTGCGACTGTACCAAGCTGATTGTA 239

QY 1769 AAGAGCTGGCGGTACAGAGGAACAGCCCCCAGCTGAGGGGGTGTGTGAATCGGACAG 1828
DB 238 AAGAGCTGGCGGTACAGAGGAACAGCCCCCAGCTGAGGGGGTGTGTGAATCGGACAG 179

QY 1829 CTCCAGCAGAGGTGTGGAGTGCAGTCTGAGGGAAGAGACATCGGCTGGACAC 1888
DB 178 CTCCAGCAGAGGTGTGGAGTGCAGTCTGAGGGAAGAGACATCGGCTGGACAC 119

QY 1889 TCAGGAGGTCAAAAGGAGACTTGTGTCACCACTCATCTGCCACCCCAAGATGCATC 1948
DB 118 TCAGGAGGTCAAAAGGAGACTTGTGTCACCACTCATCTGCCACCCCAAGATGCATC 59

QY 1949 CTGCCTCATCAGTCCAGATTTCTTTCCAAAGGGGAGCTTTCTGTGTGAAATTC 2002
DB 58 CTGCCTCATCAGTCCAGATTTCTTTCCAAAGGGGAGCTTTCTGTGTGAAATAC 5

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RESULT 2
BE549374      434 bp mRNA linear EST 09-AUG-2000
LOCUS        601074602F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460537 5',
DEFINITION   mRNA sequence.
ACCESSION    BE549374
VERSION      BE549374.1 GI:9778019
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 434)
AUTHORS      NIH-MGC
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgaabs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: Incyte Genomics, Inc.
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LHAM455 row: c column: 02
              High quality sequence stop: 432.
              Location/Qualifiers
FEATURES     source
              1. .434

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3460537"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH MGC 12"
/notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 Kb. Library prepared by Life
Technologies."
Query Match      16.5%; Score 395.2; DB 1; Length 434;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 400; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 961 GCGTTTGAAGAAACCCGGTGTATCCGACATCCAAAGCAGCTCAATAGACGATGTG 1020
DB 1 GCGTTTGAAGAAACCCGGTGTATCCGACATCCAAAGCAGCTCAATAGACGATGTG 60

QY 1021 GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGAGCCTC 1080
DB 61 GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGAGCCTC 120

QY 1081 CTATTCCCACTTGTGGAAGAGACCAATGAGAGACAGTTCGAGATTTTACATTGGAAT 1140
DB 121 CTATTCCCACTTGTGGAAGAGACCAATGAGAGACAGTTCGAGATTTTACATTGGAAT 180

QY 1141 ACAGTGCAGCTTGTGAAACTGTTCGAGAGATGTGCGGTATATGAAAAGACATCTGGG 1200
DB 181 ACCGGGACAGCTTAGTAAAGTGTTCGAGAGATGTGCGGTATATGAAAAGACATCTGGG 240

QY 1201 TTTGAGCAGTGTAAAGTGTTCGAGAGATGTGCGGTATATGAAAAGACATCTGGG 1260
DB 241 TTTGAGCAGTGTAAAGTGTTCGAGAGATGTGCGGTATATGAAAAGACATCTGGG 300

QY 1261 GAAAAGCATTCAGAAAGTCTTATCAACCTGGGCTCCAAAGTTCTCAGGAGTACCTGGAT 1320
DB 301 GAAAAGCATTCAGAAAGTCTTATCAACCTGGGCTCCAAAGTTCTCAGGAGTACCTGGAT 360

QY 1321 GCTCTGAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCAGTTC 1368
DB 361 GCTCTGAGACGCTGAGCTTGTCCCTGAGTGCACAAAGTGGCCAGTAC 408

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RESULT 3
BX377107/c    1201 bp mRNA linear EST 08-MAY-2003
LOCUS        BX377107 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION   clone CS0DI002YE24 3-PRIME, mRNA sequence.
ACCESSION    BX377107
VERSION      BX377107.1 GI:30438914
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 1201)
AUTHORS      Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL      Unpublished (2001)
COMMENT      Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              Library was constructed by Life Technologies, a division of
              Invitrogen. This sequence belongs to sequence cluster 2614.f For
              more information about this cluster, see
              http://www.genoscope.cns.fr/
              cgi-bin/cluster.cgi?seq=CS0DI002BC12NP1&cluster=2614.f. Contact :
              Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
              Faraday Avenue Genoscope sequence ID : CS0DI002BC12NP1.

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FEATURES
source

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Location/Qualifiers
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1002YE24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match      16.3%; Score 390.4; DB 1; Length 1201;
Best Local Similarity 93.8%; Pred. No. 0;
Matches 438; Conservative 4; Mismatches 21; Indels 4; Gaps 4;

Qy 1910 TTGTGTCACCA-CTCATCTCTGCCAC-CCCCAGAAATGATCTGCTCATCAGTCCAGA 1967
Db 470 TTGRTGCACCACTCATCTCTGCCACGCCAGAAATGATCTGCTCATCAGTCCAGA 411

Qy 1968 TTCTTTTCCAGGGGAC-GTTTCTGTTGGAATTTCTTAGTCTTGGCTCGGACACTT 2026
Db 410 TTCTTTTCCAGGGGACAGTTTCTGTTGGAATTTCTTAGTCTTGGCTCGGACACTT 351

Qy 2027 CATTCGTTAGTGGGAGTGTGTGGAGGAGTGAAGAGGCGGATGTCACACTCAG 2086
Db 350 CATTCGTTAGTGGGAGTGTGTGGAGGAGTGAAGAGGCGGATGTCACACTCAG 291

Qy 2087 ATCCACAGAGCCCAAGGATCAAGGAGCCACTGTCAGTGGCAGCAGACTGTTGGGCCCCCA 2146
Db 290 ATCCACAGAGCCCAAGGATCAAGGAGCCACTGTCAGTGGCAGCAGACTGTTGGGCCCCCA 231

Qy 2147 CCCCACCTTGCAGAGCCCTCATCCCTCTTGGCTTGGCGGTGAGCGCTGCTGCTGA 2206
Db 230 CCCCACCTTGCAGAGCCCTCATCCCTCTTGGCTTGGCGGTGAGCGCTGCTGCTGA 171

Qy 2207 GTGTCTCAGCAGACACTCAGCTTGTGATCAGGCGCAGAGCTTCTCGGAGCCAGGA 2266
Db 170 GTGTCTCAGCAGACACTCAGCTTGTGATCAGGCGCAGAGCTTCTCGGAGCCAGGA 111

Qy 2267 TGATCTGTCCAGCTTGCACCTCGGCGCCATCTCGGCTCATGCTCTCTCTCTCTCTATT 2326
Db 110 TGATCTGTCCAGCTTGCACCTCGGCGCCATCTCGGCTCATGCTCTCTCTCTCTATT 51

Qy 2327 GAATTAGTAC-CTAGTGCACACAGTATGATTTACCAAAAGATAA 2372
Db 50 GAATTAGTACNTGNCGACACAGTATGATTTACCAAAAGATAA 4

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RESULT 4

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BX097186/c      390 bp      mRNA      linear      EST 04-FEB-2003
LOCUS           BX097186
DEFINITION      BX097186 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE998A055391 ;
IMAGE:2181772, mRNA sequence.
ACCESSION       BX097186
VERSION         BX097186.1 GI:27828694
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 390)
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
Human UnigeneSet - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE998A055391.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)

```

```

http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel.: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (Clone@rzpd.de) for further information. Seq primer:
M13u, Primer sequence: CGTTGTAACAGCAGGCGCAT.
FEATURES
Location/Qualifiers
1. 390
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE998A055391 ; IMAGE:2181772"
/tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ut4"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"

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FEATURES
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Query Match      15.5%; Score 371.8; DB 1; Length 390;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 376; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2011 TGGCTCGGACACTTCATTCTGTTAGCTGGGAGTGTGTGAGGAGTGAAGAGGCG 2070
Db 390 TGGCTCGGACACTTCATTCTGTTAGCTGGGAGTGTGTGAGGAGTGAAGAGGCG 331

Qy 2071 GATGTGTACACTCAGATCCACAGAGCCAGGATCAAGGAGCCACTGTCAGTGCACAG 2130
Db 330 GATGTGTACACTCAGATCCACAGAGCCAGGATCAAGGAGCCACTGTCAGTGCACAG 271

Qy 2131 GACTGTTGGGCCCCCAACCCCAACCCCTGTCAGAGCCCTCATCCCTCTTGGCTTGAAGCGTC 2190
Db 270 GACTGTTGGGCCCCCAACCCCAACCCCTGTCAGAGCCCTCATCCCTCTTGGCTTGAAGCGTC 211

Qy 2191 AGAGGCGCTGTGTGAGTGTGTGACCGAGACACTCAGCTTGTTCATCAGGGCACAGGC 2250
Db 210 AGAGGCGCTGTGTGAGTGTGTGACCGAGACACTCAGCTTGTTCATCAGGGCACAGGC 151

Qy 2251 TTCTCTGGAGCCAGGATGATCTGTGCCACCTTGCACCTCGGCCCATCTGGGCTCATGC 2310
Db 150 TTCTCTGGAGCCAGGATGATCTGTGCCACCTTGCACCTCGGCCCATCTGGGCTCATGC 91

Qy 2311 TCTCTCTCTGCTATTGAATTAGTACCTAGTCACACAGTATGTAGTTACCAAGAAAT 2370
Db 90 TCTCTCTCTGCTATTGAATTAGTACCTAGTCACACAGTATGTAGTTACCAAGAAAT 31

Qy 2371 AAACGGCAATAATTGAGAAAAAAA 2395
Db 30 AAACGGCAATAATTGAGAAAAAAA 6

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RESULT 5

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BU425116      640 bp      mRNA      linear      EST 29-NOV-2002
LOCUS           BU425116
DEFINITION      603962196F1 CSEQRN09 Gallus gallus cDNA clone ChEST939023 5', mRNA
sequence.
ACCESSION       BU425116
VERSION         BU425116.1 GI:25917792
KEYWORDS        EST.
SOURCE          Gallus gallus (chicken)
ORGANISM        Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 640)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,

```

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .640
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST939023"
/sex="Male and female"
/tissue type="Chondrocytes isolated from growth plate cartilage"
/dev stage="adult"
/lab_host="DH108"
/clone_lib="CSQREN09"
/note="Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
15.5%; Score 371.8; DB 1; Length 640;
Best Local Similarity 76.1%; Pred. No. 0;
Matches 481; Conservative 0; Mismatches 149; Indels 2; Gaps 2;
QY 208 CCCCCAGCGCCGACCCCTGGCTGGCGGACGAGTCTTAACCTGGACACCGCTGCCACCACT 267
DB 10 CGCCGAGCGCGCCGCGCCGACGAGTCTTAACCTGGACACCGCTGCCACCACT 69
QY 268 CTCCTCAGTAAAGTTGTTATGTTCTGATAGATGCTTGGAGATGATTTTGTGTTGG 327
DB 70 CTTTTCAGAAAGTTGTGTCGTTCTGTATAGATG-CTTGAGATGATTTTGTCTTTGA 128
QY 328 TCAAGGGTGTGAATTTATGCTCTACACAACTTACTTGTGAAAGAGGAGCATCTCAC 387
DB 129 TCCAAAGTTAAACAGTTTCAGCTTACCTACACAGTATTGAAAGGAGCTTCTTAC 198
QY 388 AGTTTGTGGCTGAAGCAAGCCACCTACAGTTACTATGCTCGAATCAAGGATGATG 447
DB 189 AGTTTCATGCTGAAGCAAGCCACCGCTGACTATGCTCGAATTAAGGCTTTGATG 248
QY 448 ACGGGAGCGCTTCTGCTTGTGCGAGCTCATCAGGAACCTCAATTTCTCTGCACTGCTG 507
DB 249 ACGGGTAGCATTTCTGTTTTCATTTGATGTTGTTGTAACCTCACTCCAGCTCTGATG 308
QY 508 GAAGACAGTGTGATGACAGCAAGCAAGAGCAGCTGGAAAAAGAAATAGTCTTTTATGAGAT 567
DB 309 AGTGACATCTGATATGCGCAAGCAAGAGCAGCTGGGAAAAAGAAATATCTTTTACGGTGT 368
QY 568 GAAACCTGGGTTAAATTTATTTCCCAAGCATTTTGTGGAATATGATGGAACAACTCATTT 627
DB 369 GATACCTTGGGTAAATTTGTTTCCAAAGCA-TTTGTGGAATATGATGGAACCAAGCTCCTTT 427

Query Match 15.5%; Score 371.8; DB 1; Length 640;
Best Local Similarity 76.1%; Pred. No. 0;
Matches 481; Conservative 0; Mismatches 149; Indels 2; Gaps 2;

FEATURES source
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/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="CHEST939023"
/sex="Male and female"
/tissue type="Chondrocytes isolated from growth plate cartilage"
/dev stage="adult"
/lab_host="DH108"
/clone_lib="CSQREN09"
/note="Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

QY 628 TTCGTGTCAGATTACACAGAGTGTGATAATAATGTCAAGGCGCATTTTGATAAAGTATTA 687
DB 428 TTCGTGTCAGATTATTTACAGAGTTGATGATTAATGTTACTACACATTTGGATAGAGTTG 487
QY 688 AAAAGAGGAGATTGGGACATATTAACTCCTACCTACCTGGGGCTGGACCAATTGGCCAC 747
DB 488 AAGAGAGAGGAGTGGGATCTCTTAATATTACATTACCTAGGATNGGACCATATNGGACAT 547
QY 748 ATTTTCAGGGCCCAACAGAGCCCTGATTTGGGAGAGCTGAGGAGATGAGACAGCTGCTG 807
DB 548 ATGACTGGGCGCAACAGAGCCCTGCTGGGACCAAGCTTCGTGAAATGCAACACGCTCTG 607
QY 808 ATGAAGATCCACACCTCACTGCGAGTCGAAGA 839
DB 608 AAGAAGATTCAATTTCTGCTGTCAAGA 639

RESULT 6
BG336024 920 bp mRNA linear EST 27-FEB-2001
LOCUS 602404781F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4542237 5',
DEFINITION mRNA sequence.
ACCESSION BG336024
VERSION BG336024.1 GI:13142462
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 920)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1222 row: a column: 22
High quality sequence stop: 573.
High quality sequence stop: 573.

FEATURES source
1. .920
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4542237"
/tissue type="choriocarcinoma"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 14.9%; Score 356.7; DB 1; Length 920;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 380; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

QY 54 CCGCATCCAGCTTAGCGTGTCCACGATGGCTGGGCTCGGACCTTCGCTACCTGTTG 113
DB 2 CCGCATCCAGCTTAGCGTGTCCACGATGGCTGGGCTCGGACCTTCGCTACCTGTTG 61
QY 114 CGTAGCGATCGAGTGTCTAGGATCGGCTTCCTTCGGGGATTCCTCCGGCTCCCGT 173
DB 62 CGTAGCGATCGAGTGTCTAGGATCGGCTTCCTTCGGGGATTCCTCCGGCTCCCGT 121

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QY 174 TCGTTCCCTCTGCAGAGCGGAACACGAGCGGAGCCCGCCAGCGCCGACCCCTCGGCTGG 233
Db 122 TCGTTCCCTCTGCAGAGCGGAACACGAGCGGAGCCCGCCAGCGCCGACCCCTCGG-TGG 180
QY 234 AGCCAGTTCCTAACTGAGCAGCAGCTGCGACCACTCTCTTTCAGTAAAGTGTGTAATGTTCT 293
Db 181 AGCCAGTTCCTAACTGAGCAGCAGCTGCGACCACTCTCTTTCAGTAAAGTGTGTAATGTTCT 240
QY 294 GATAGATGCTTTCAGAGATGATTTTGTGTTGGGTCAAAAGGTGTGAATTTATGCCCTTA 353
Db 241 GATAGATGCTTTCAGAGATGATTTTGTGTTGGGTCAAAAGGTGTGAATTTATGCCCTTA 298
QY 354 CACAACTTACCTTGTGGAAGGAGGAGCATCTCACAGTTTGTGCTGGAAGCAAGCCACC 413
Db 299 CACAACTTACCTTGTGGAAGGAGGAGCATCTCACAGTTTGTGCTGGAAGCAAGCCACC 358
QY 414 TACAGTTACTATGCTCGAATCAAGG 439
Db 359 TACAGTTACTATGCTCGAATCAAGG 384

RESULT 7
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LOCUS 602405340F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4542968 5',
DEFINITION mRNA sequence.
ACCESSION BG336399
VERSION BG336399.1 GI:13142837
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 970)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: rcapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHCMI223 row: p column: 09
High quality sequence stop: 661.
FEATURES
Location/Qualifiers
1..970
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4542968"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Query Match 14.9%; Score 356.7; DB 1; Length 970;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 380; Conservative 0; Mismatches 3; Indels 3; Gaps 2;
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QY 54 CCGCATCCAGCCTAGCGTGTCCACGATGCGGCTCGGACTTCGCTACCTGTTG 113
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Db 2 CCGCATCCAGCCTAGCGTGTCCACGATGCGGCTCGGCTCGGACTTTCGCTACCTGTTG 61
QY 114 CCGTAGCGATCCGAGGTGCTAGGATCGCGTCTTCTTCGGGATTTCTCCCGGCTCCCGT 173
Db 62 CGTAGCGATCCGAGGTGCTAGGATCGCGTCTTCTTCGGGATTTCTCCCGGCTCCCGT 121
QY 174 TCGTTCCCTCTGCAGAGCGGAACACGAGCGGAGCCCGCCAGCGCCGACCCCTCGGCTGG 233
Db 122 TCGTTCCCTCTGCAGAGCGGAACACGAGCGGAGCCCGCCAGCGCCGACCCCTCGGCTGG 181
QY 234 AGCCAGTTCCTAACTGAGCAGCAGCTGCGACCACTCTCTTTCAGTAAAGTGTGTAATGTTCT 293
Db 182 AGCCAGTTCCTAACTGAGCAGCAGCTGCGACCACTCTCTTTCAGTAAAGTGTGTAATGTTCT 241
QY 294 GATAGATGCTTTCAGAGATGATTTTGTGTTGGGTCAAAAGGTGTGAATTTATGCCCTTA 353
Db 242 GATAGATGCTTTCAGAGATGATTTTGTGTTGGGTCAAAAGGTGTGAATTTATGCCCTTA 299
QY 354 CACAACTTACCTTGTGGAAGGAGGAGCATCTCACAGTTTGTGCTGGAAGCAAGCCACC 413
Db 300 CACAACTTACCTTGTGGAAGGAGGAGCATCTCACAGTTTGTGCTGGAAGCAAGCCACC 358
QY 414 TACAGTTACTATGCTCGAATCAAGG 439
Db 359 TACAGTTACTATGCTCGAATCAAGG 384
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RESULT 8
BG927822 674 bp mRNA linear EST 06-NOV-2001
LOCUS HNC7-1-B4.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION sequence.
ACCESSION BG927822
VERSION BG927822.1 GI:14322345
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 674)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
JOURNAL 21482651
MEDLINE 11597177
PUBMED
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.
FEATURES
Location/Qualifiers
1..674
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/mol_type="mRNA"
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Directional"
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Query Match 14.2%; Score 340.5; DB 1; Length 674;
Best Local Similarity 72.5%; Pred. No. 0;
Matches 434; Conservative 0; Mismatches 10; Indels 155; Gaps 1;
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QY 1352 CACAAGTGGCCAGTTTCTCACCTCTCTGCTCAGCGTCCACAGGCACTGCACAGAA 1411
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Db 76 CACGCGTCCGCGAGTTCTCACCCCTGCTCCTGCTAGCGTCCACAGGCACTGCGCAGAAA 135
Qy 1412 GGCTGAGCTGGAAGTCCCACTGCTATCTCTCGGTTTCTCTGCTCTTTTATTTGGTGAT 1471
Db 136 GGCTGAGCTGGAAGTCCCACTGCTATCTCTCGGTTTCTCTGCTCTTTTATTTGGTGAT 195
Qy 1472 CTTGTTCTTTTCCGCGGTTTCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1531
Db 196 CTTGTTCTTTTCCGCGGTTTCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 255
Qy 1532 CTGTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1554
Db 256 CTGTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 315
Qy 1555 ----- 1554
Db 316 TGTGATTGTTCTGTTCTGACCAACGTGCTGCTGGTGGTGGAAACACCCCAAGGAGTAGC 375
Qy 1555 -----CA 1556
Db 376 TACGGCTGTTTCTGCGAGTGTGACGTAGTCTCTCTGCTCAGGTTGTTCTGTTATTCTCA 435
Qy 1557 GGCTGCTTTCTTTTACAGACTCTGTTGAAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1616
Db 436 GGCTGCTTTCTTTTACAGACTCTGTTGAAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
Qy 1617 GGCCTGGACAGGGGGCTCTCAGGGAAGAGCTGGAGCAGCTTATCCAGGCTCTGGGTG 1676
Db 496 GGCCTGGACAGGGGGCTCTCAGGGAAGAGCTGGAGCAGCTTATCCAGGCTCTGGGTG 555
Qy 1677 TCCCGACAGGTTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1736
Db 556 TCCCGACAGGTTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615
Qy 1737 AGTTTCTGCGACTGTTTACCAAGTGATTTGTAAGAGCTGGCGTCCACAGAGGAAACAAG 1795
Db 616 AGTTTCTGCGACTGTTTACCAAGTGATTTGTAAGAGCTGGCGTCCACAGAGGAAACAAG 674

RESULT 9
LOCUS BE757899 557 bp mRNA linear EST 25-APR-2001
DEFINITION 212468-MARC 2BOV Bos taurus cdna 5', mRNA sequence.
ACCESSION BE757899.1 GI:10171891
VERSION BE757899.1
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 557)
Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Perle, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keesle, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cdna
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers

FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCCAGAG
Plate: 65 row: K column: 17
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
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/tissue_type="pooled"
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/clone_lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
Query Match 14.1%; Score 338; DB 1; Length 557;
Best Local Similarity 87.2%; Pred. No. 0;
Matches 381; Conservative 0; Mismatches 50; Indels 6; Gaps 1;
QY 62 AGCTAGAGTGTTCACAGATGCGGCTCGGCTCGGACCTTCCTGCTACCTGTTGGTAGCA 121
DB 126 AGCGAGGGTGGGACGATGCGGCTCGGCTCGGACCTTCCTGCTCGGCTCGGCTCGG 185
QY 122 TCAGAGTGTCTAGGATCGGCTCTTCTTTCGGGGATTCCTCCGGCTCCCGTTCTCT 181
DB 186 TCAGAGTGTCTCGGCTCGGCTCTTCTTTCGGGGATTCCTCCGGCTCCCGTTCTCT 239
QY 182 CTGCCAGAGCGGAAACACGAGCGGAGCCGCCAGCGCCGAAACCTCGGCTGAGCCAGTT 241
DB 240 TTTCCGGAGCGGAGCGGAAACGAGAGTCCCGCGCCGAAACCTCTGCTGAGCCAGTT 299
QY 242 CTAACTGAGACCGCTGCGACCACTCTCTTCTAGTAAAGTTGTTATTGTTGATAGTG 301
DB 300 CCAACTGGACCGAGCTTCCACCACCGCTCTTCTAGTAAAGTTGTTATTGTTGATAGTG 359
QY 302 CTTGAGAGATGATTTTGTGTTTGGTCAAAGGCTGTAATTTATGCTTACCAACTT 361
DB 360 CTTGAGAGATGATTTTGTGTTTGGATCAAAGGCTGTAATTTATGCTTACCAACTT 419
QY 362 ACCTTGTGAAAAGAGAGATCTCAGATTTTGTGCTGAGCAAGCAAGCCCTACAGTTA 421
DB 420 ATCTTGTGAAAAGAGATCTCAGATTTTGTGCTGAGCAAGCAAGCCCTACAGTTA 479
QY 422 CTATGCTCGATCAAGGATTCATGACGGGAGCGCTTCTGCTGTTGTCAGCTCATCA 481
DB 480 CTATGCTCGATCAAGGCGTCTGACAGGAGCGCTTCTGCTGTTGTCAGCTCATCA 539
QY 482 GGAACCTCAATTCTCTCT 498
DB 540 GGAACCTCAATTCTCTCT 556

RESULT 10
LOCUS AW262524/c 368 bp mRNA linear EST 28-DEC-1999
DEFINITION qx8510.x1 NCI CGAP Brn53 Homo sapiens cdna clone IMAGE:2757451.3
similar to SW:7A93_SCHPO Q09782 HYPOTHETICAL 85.7 KD PROTEIN
C13G6.03 IN CHROMOSOME 1.; mRNA sequence.
ACCESSION AW262524
VERSION AW262524.1 GI:6639340
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 368)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/Brn53), Tumor Gene Index
Unpublished (1998)
JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html
 Seq primer: -400P from Gibco
 High quality sequence stop: 368.
 Location/Qualifiers
 1. 368

FEATURES

source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2757451"
 /tissue_type="three pooled meningiomas"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Brn53"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."

Query Match

Best Local Similarity 13.1%; Score 314.2; DB 1; Length 368;
 Matches 358; Conservative 0; Mismatches 3; Indels 4; Gaps 4;
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 Db |||||
 Qy 362 TTGGTCAAGGGTGT-AAAATTATGCCCTACACAACTTACCTTGTG-AAAAGGAGCAT 305
 Db |||||
 Qy 383 CTCACAGTTTGTGGCTGAAGCAAGCCACCTACA-GTTACTATGCTTCGTAATCAAGGCA 441
 Db |||||
 Qy 304 CTCACAGTTTG-GGCTGAAGCAAGCCACCTACAGGTTACTATGCTTCGTAATCAAGGCA 246
 Db |||||
 Qy 442 TTGATGACGGGAGCGTTCCTGGCTTTGTGACGTCATCAGGAACCTCAATCTCCTGCA 501
 Db |||||
 Qy 245 TTGATGACGGGAGCGTTCCTGGCTTTGTGACGTCATCAGGAACCTCAATCTCCTGCA 186
 Qy 502 CTGCTGAAGACAGTGTGATAAGCAAGCAAAAGCAGCTGGAAGAAAGTAAGTCTTTAT 561
 Db |||||
 Qy 185 CTGCTGAAGACAGTGTGATAAGCAAGCAAAAGCAGCTGGAAGAAAGTAAGTCTTTAT 126
 Qy 562 GGAGATGAACCTGGGTAAATTTATCCCAAGCAATTTGTGGAATATGATGGAACAACC 621
 Db |||||
 Qy 125 GGAGATGAACCTGGGTAAATTTATCCCAAGCAATTTGTGGAATATGATGGAACAACC 66
 Qy 622 TCATTTTTCGTGTGATGATACACAGAGTGGATAATATATGTCAGAGGCATTTGGATAAA 681
 Db |||||
 Qy 65 TCATTTTTCGTGTGATGATACACAGAGTGGATAATATATGTCAGAGGCATTTGGATAAA 6
 Qy 682 GTATT 686
 Db |||||
 5 GTATT 1

RESULT 11

BM844459

LOCUS

BM844459 332 bp mRNA linear EST 06-MAR-2002
 K-EST0122574 S13KMS5 Homo sapiens cDNA clone S13KMS5-36-B11 5', mRNA sequence.

ACCESSION

BM844459

VERSION

BM844459.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 332)

AUTHORS

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

TITLE

JOURNAL

COMMENT

Kim, Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 36 row: B column: 11
 High quality sequence stop: 332.
 Location/Qualifiers
 1. 332

FEATURES

source

/organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="S13KMS5-36-B11"
 /tissue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10P"
 /clone_lib="S13KMS5"
 /note="Vector: pCMS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

Query Match

Best Local Similarity 12.9%; Score 309.7; DB 1; Length 332;
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 Qy 8 CAGCTCCCTTTCTGTTT-CCAGACTCTGGTTGAACACTGGTGTGTCACAGTCTGSCA 66
 Qy 1615 GTGCCCTGGACAGGGGCTCAGGAAGAGCCTGGAGCAGCTTATCCAGGCTCTGGG 1674
 Db |||||
 Qy 67 GTGCCCTGGACAGGGGCTCAGGAAGAGCCTGGAGCAGCTTATCCAGGCTCTGGG 126
 Qy 1675 TGTCCCGACACAGAGTGTTCACATCTGTCGTGTCAGGTCAGATGCCTCAGTCTTGGAAAG 1734
 Db |||||
 Qy 127 TGTCCCGACACAGAGTGTTCACATCTGTCGTGTCAGGTCAGATGCCTCAGTCTTGGAAAG 186
 Qy 1735 CTAGGTTCTTCCGACTGTTTACCAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAA 1794
 Db |||||
 Qy 187 CTAGGTTCTTCCGACTGTTTACCAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAA 246
 Qy 1795 GCCCCCCAGCTGAGGGGGTGTGTGTAATCGACACGCTCCAGCAGAGGTGTGGAGCTGC 1854
 Db |||||
 Qy 247 GCCCCCCCGCTGAGGGGGTGTGTGTAATCGACACGCTCCAGCAGAGGTGTGGAGCTGC 306
 Qy 1855 AGCTGAGGGAAGAGAGACAATCGGC 1880
 Db |||||
 307 AGCTGAGGGAAGAGAGACAATCGGC 332

RESULT 12

BG346870

LOCUS

BG346870 595 bp mRNA linear EST 28-FEB-2001
 dad16902.y1 Wellcome CRC PCS107 tropicalis Str10-12 Silurana tropicalis cDNA clone IMAGE:4439978 5' similar to SW:YA93_SCHPO

Q09782 HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I. ;,
mRNA sequence.
BG346870
BG346870.1 GI:13167294
EST.
Silurana tropicalis (western clawed frog)
Silurana tropicalis
Silurana tropicalis
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodidae; Silurana.
1 (bases 1 to 595)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L.,
Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y.,
Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,I., McCann,R.,
Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
Unpublished (1999)
Contact: Sandy Clifton, Ph.D.

WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1310
Email: est@watson.wustl.edu
Library constructed by A. Zorn and J. Mason (Wellcome/CRC
Institute). DNA Sequencing by: Washington University Genome
Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LINL at: info@image.lnlnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 492.

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FEATURES
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1..595
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/mol_type="mRNA"
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/clone_lib="Wellcome CRC pCS107"
/notes="vector: pCS107; Site 1: NotI; Site 2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Average insert size 1.5 kb, range 0.5-4 kb. Library constructed by Dr. Jason Wellcome (CPC Institute)."

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Query Match	12.9%;	Score 308.9;	DB 1;	Length 595;
Best Local Similarity	72.5%;	Pred. No. 0;		
Matches 413;	Conservative 0;	Mismatches 156;	Indels 1;	Gaps 17;
QY	248	GGACGAGCTGCGACCACTCTCTTCAGTAAAGTTGTTATTGTTCTGTAGATGCGCTTGA	307	
Db	6	GGACAAACATTCCTTCACCTCTTTTCAAAAAAGTTGTCGTCTCTTAATCGATGCTTTGA	65	
QY	308	GAGATGATTTTGCTTTGGGTCAAGGGTGTGAATTTATGCCCTACACAACTTACCTTG	367	
Db	66	GACAGGACTTTGTGTATGGTCCAAAGGGGGAAGAACATATGCTTACCTTACCCAACTTG	125	
QY	368	TGGAAAAAGGAGCATCTCACAGTTTGTGGCTGGAAGCAAAAGCCACTCAGTTTACTATGC	427	
Db	126	TAGAAAAGGAACAAACACACAGTTCATAGCAAAAGCAGCAGCTCCACTGTCCACCATGC	185	
QY	428	CTCGAATCAAGGCATTTGATGACGGGGAGCCCTTCCTGGCTTTGTGCAAGCTCATCAGAAC	487	
Db	186	CTCGTATCAAGCCCTGATGACAGGTAGCATCCCTGGATTTATTGATGTTGTAATGAATC	245	
QY	488	TCAATTTCTCTGCACTGCTGGAAAGACAGTGTGATTAAGACACAGCAAAAGCAGCTGGAAAA	547	
Db	246	TAAATTCAACGAATTACTGGATGACAATGTGATATGGCAAGGAAAGCAAGCTGGAAAA	305	
QY	548	GAATAGCTTTTATGGAGATGA-AACCTGGGTTTAAATTTATCCCAAGACATTTTGTGAA	606	
Db	306	GGATAGTATTTTATGGAGATGATACTTGATTAAGACTTTTCCCAAAATTTTGTCTGAA	365	

607	QY	TATGATGGACAACTCATTTTCGTGTCAGATTACACAGAGGTGGATATAATGTCACG	666
366	Db	TATGATGGAACAACATCATTTTTGTTCTGATTATACAGAGGTGGATATAATGTTACA	425
667	QY	AGGCATTTGGATAAAGTATTTAAAAGAGGAGATTGGGCATATTAATTCCTCCACTACCTG	726
426	Db	AGGCATTTTGATGATATATTTAAAGAGAAATGACTGGGATATGCTTATCCTTCATCTCTT	485
727	QY	GGGCTGGACCAATTTGGCCACATTTTCAGGCGCCAAACAGCCCTCGATTGGCGGAGAACCTG	786
486	Db	GGATTAGATCATAGGACATTTTAACAGGACCACATAGTCATTTAATCGTGCCAAAACCTT	545
787	QY	AGCGAGATGACAGCGTGCTGATGAAGATC	816
546	Db	CTTGAATGGACACTGTCTCTTAATAAAAAAATC	575

RESULT 13
AW262485/c
LOCUS
AW262485 405 bp mRNA linear
DEFINITION
xq85all.x1 NCI CGAP Btn53 Homo sapiens cDNA clone IMAGE:2757404 3'
similar to SW:A93_SCHPO Q09782 HYPOTHETICAL 85.7 KD PROTEIN
C13G5_03 IN CHROMOSOME I.; mRNA sequence.
EST 28-DEC-1999

Accession
Version
Keywords
Source

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 405)
REFERENCE

NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGA), Tumor Gene Index
Unpublished (1998)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center

Genome sequencing center.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 955.

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FEATURES
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Location/Qualifiers
1..405
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2757404"
/tissue_type="three pooled meningiomas"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn53"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies."

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Query Match	12.8%	Score 305.6	DB 1	Length 405
Best Local Similarity	91.0%	Pred. NO. 0		
Matches 355; Conservative		0	Mismatches 31	Indels 4
				Gaps 3

Qy 301 GCCTTGGAGAGATGATTTTGTGTTGGGTCAAAGGGTGTGAATTTATGCCCTACACA-AC 359

Db 390 GCCTTGGAGAGATGATTTTGTGTTGGGTCAAGGGTGTGAATTTNAATGCCCTACACANAC 331

Qy 360 TTACCTTGTGGAAAAAGAGACATCTCACAGTTTTTGGCTGAAGCAAGACCCACCTAC--A 417

Db 330 TTTTACTGGTGTAAAAAGAGACATCTCACAGTTTGTGGCTGAAGCAAGAAAGCCCTACCAAG 271

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QY 418 GTTACTATGCTCGAATCAAGGCAATGATGACGGG-GAGCCTTCCTGGCTTTGTGCGAGT 476
Db 270 GTTACTATGCTTCGAATCAAGGCAATGATGACGGGNGAGCCCTTCCTGGCTTTGTGCGAGT 211
QY 477 CATCAGGAACTCAATTCCTCGCACTGCTGGAAGACAGTGTGATAAGACAAAGC 536
Db 210 CATCAGGAACTCAATTCCTCGCACTGCTGGAAGACAGTGTGATAAGACAAAGC 151
QY 537 AGCTGGAAGAAAGATAGTCTTTTATGGAGATGAGAACCTCGGTTAAATATTATCCCAAAGCA 596
Db 150 AGCTGGAAGAAAGATAGTCTTTTATGGAGATGAGAACCTCGGTTAAATATTATCCCAAAGCA 91
QY 597 TTTTGTGGAATATGATGGAACAACCTCAATTTTTCGTGCAGATTACAGAGGTGATAA 656
Db 90 TTTTGTGGAATATGATGGAACAACCTCAATTTTTCGTGCAGATTACAGAGGTGATAA 31
QY 657 TAAATGTACGAGGCAATTTGGATAAGTATT 686
Db 30 TAAATGTACGAGGCAATTTGGATAAGTATT 1

RESULT 14
LOCUS BE669243
DEFINITION BE669243 570 bp mRNA linear EST 08-SEP-2000
5' similar to SW:YA93 SCHPO Q09782 HYPOTHETICAL 85.7 KD PROTEIN
C33G6.03 IN CHROMOSOME 1.; mRNA sequence.
ACCESSION BE669243
VERSION BE669243.1 GI:10029719
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 570)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other ESTs: dc59c11.x1
Contact: Robert Strausberg, Ph.D.
Email: c9apbs@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LINL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 420.
FEATURES
Location/Qualifiers
1..570
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:3401396"
/tissue_type="embryo (stage 10)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_XGC Embl"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 1.55 kb. Constructed by Life Technologies. Note: this
is a Xenopus Gene Collection (XGC) library."
Query Match 12.7%; Score 304; DB 1; Length 570;
Best Local Similarity 71.0%; Pred. No. 0;
Matches 403; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
QY 245 ACTGCACACGCTGCCACCACTCTCTTCAGTAAGTTGTTATGTTCTGATAGATGCT 304
Db 2 ACGGTCCGCACATCTCCACCTCTCTTCAGTAAGTTGTTATGTTCTGATAGATGCT 61

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QY 305 TGAGAGATGATTTTGTGTTGGTCAAAAGGGTGTGAAATTTTATGCCTACACAACTTACC 364
Db 62 TAAGACAGGACTTTGTGTATGTCCTCAAGGGGAAGACATATGCTTACCTTACACAAAC 121
QY 365 TTGTGGAAGAAAGGAGCATCTCAGTTTGTGGCTGGAAGCAAGCCACCTACAGTTACTTA 424
Db 122 TTTTGGAAAAAGGAACAACACATAGCTTCTAGCAAAAAGCCACAGCAACCACTGTCACTA 181
425 TGCCTCGAATCAAGGCAATGATGACGGGGAGCCTTCCTGGCTTTGTGCGAGTCATCAGA 484
Db 182 TGCCTCGTATCAAGGCCCTTAATGACAGGTGATCCAGGATTCATGATGTTGTAATGA 241
485 ACCTCAATTCCTGCACTGCTGGAAGACAGTGTGATAAGCAACAAGCAGCTGGAA 544
Db 242 ATCTAAATTCACAGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 301
545 AAAGNATAGTCTTTTATGGAGATGAAACCTGGGTTAAATTTATCCCAAGCAATTTGTGG 604
Db 302 AACGTATAGTATTTTATGGAGATGATCTTGGATAAGACTTTTCCCAAAACATTTTCTG 361
605 AATATGATGGAACAACCTCATTTTTCGTGTCAGATTACACAGAGTGTGATAATATGTCA 664
Db 362 AATATGATGGAACCTACATCATTTTTCGTGATTATACAGAGTGTGATAATATGTCA 421
665 CGAGGCAATTTGGATAAGTATTAAGAGAGGAGATTTGGACATATTAATCTCCACATACC 724
Db 422 CAAGGCACCTTGGATGACATATTAAGAGGAATGATGATGATGATGATGATGATGATGAT 481
725 TGGGCTGGACCAATTTGGCCACATTTTCAGGGCCCAACAGCCCCCTGATGGGAGAGC 784
Db 482 TTGATTAGATCATACATAGGACATTTTAAACAGGACCACATAGTCATTTAGTCGGTCCAAAAC 541
785 TGAGCGAGATGAGCAGCGTCTGATGAA 812
QY 542 TTCTTGAATGGACACTGTCCTAAGAA 569
Db

CA377408 739 bp mRNA linear EST 06-NOV-2002
655979 NCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT39002_C_H01 5',
mRNA sequence.
CA377408
CA377408.1 GI:24696413
EST.
Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 739)
Rexroad, C.E. and Keele, J.W.
Sequence analysis of a rainbow trout normalized cDNA library
Unpublished (2002)
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by
cross_match v0.990329.
Seq primer: AGCGGATACCAATTTCCACACAGCA.
FEATURES
Location/Qualifiers
1..739
/organism="Oncorhynchus mykiss"
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/clone="1RT39002_C_H01"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="NCCWA 1RT"

```



```

REFERENCE
AUTHORS   Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
          Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
          Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
          Chitko-McKown, C.G., Perlea, G., Holt, I., Karanycheva, S., Liang, F.,
          Quackenbush, J., and Keefe, J.W.
TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
          libraries and construction of a gene index for cattle
JOURNAL   Genome Res. 11 (4), 626-630 (2001)
MEDLINE   21180013
PUBMED   11282978
COMMENT   Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called and alt trimmed with phred
          v0.980904.e. Vector identified by cross_match with the -minscore 18
          and -minmatch 12 options.
          PCR Primers
          FORWARD: AGGAACAGCTATGACCAT
          BACKWARD: GTTTCACGTCAGCAGC
          Place: 108 row: P column: 21
          Seq primer: ATTAGTGACACTATAG.
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            /mol_type="mRNA"
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            /clone_lib="MARC 3BOV"
            /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
            Library made from pooled tissue from marrow, alveolar
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            longissimus muscle."
          12.3%; Score 295.6; DB 1; Length 412;
          Best Local Similarity 86.3%; Pred. No. 0;
          Matches 359; Conservative 0; Mismatches 49; Indels 8; Gaps 3;
          QY 67 AGCGTGCCACGATCGCGCTGGCTCCGGG-ACATTGCGTACCTGTGCGTAG-CGATCG 124
          Db 3 AGGCTGGGCACATGCGGCTGGGCTCCGGGTACCTTCGCTGCCACTGCGTCGATGATCG 62
          QY 125 AGGTGCTAGGATCGCGCTCTTCTTCGGGGATTTCTCCGGGCTCCGGTTCGTTCCCTCTG 184
          Db 63 AGGTCTCGGGTTCGGGCTCTTCTTCGGGGCTCTTCTCCGGGCTCCCGT-----CTTTT 116
          QY 185 CCAGAGCGGAACACGAGCGGAGCGCCCGCCAGCGCCGAGCCCTCGGTGGAGCCAGTTCTA 244
          Db 117 CCGAGCGGAGCGGCAAGCAGAGTCCCCCGGCCCGCAACCCCTGTGCTGGAGCCAGTTCCA 176
          QY 245 ACTGACCACGCTGCCACCACTCTCTTCAAGTAAAGTTGTTATTTCTCATAGATGSCCT 304
          Db 177 ACTGGACCGAGCTCCACCAACCGCTCTTCAAGTAAAGTTGTTATTTCTCATAGATGSCCT 236
          QY 305 TGAGATGATGATTTTGTGTGTTGGTCAAGAGGTGAAATTTATGCCCTACACAACTTACC 364
          Db 237 TGAGATGATGATTTTGTGTGTTGGATCAAGAGGTGAAATTTATGCCCTACACAACTTATC 296
          QY 365 TTGTGAAAAGAGGAGCATCTCAGATTTTGTGGCTGAGCAAGCCAGCCACTACAGTTACTA 424
          Db 297 TTGTGAAAAGAGGATCATCTCTCAGTTTGTGGCTGAAGCAAGCCACCTACAGTTACTA 356
          QY 425 TGCCTCGAATCAAGGATGATGACGGGAGCGCTTCTCGCTTTGTGCGAGCTATC 480
          Db 357 TGCCTCGAATCAAGGCTTGTGTCAGAGGAGCGCTTCTCGCTTTCATCGATGCTC 412
          RESULT 18
          B1919095

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LOCUS     B1919095
DEFINITION 603181038F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245209 5',
          mRNA sequence.
ACCESSION  B1919095
VERSION     B1919095.1 GI:16200149
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 753)
AUTHORS    NIH-MGC http://mgc.mci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11618 row: 1 column: 10
            High quality sequence start: 5
            High quality sequence stop: 737.
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            /db_xref="taxon:9606"
            /clone="IMAGE:5245209"
            /lab_host="DH10B"
            /clone_lib="NIH_MGC_121"
            /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
            fetal brains, female age 20 weeks, female age 24 weeks,
            and male age 26 weeks. Library is oligo-dT primed and
            directionally cloned (EcoRV site is destroyed upon
            cloning). Average insert size 1.7 kb, insert size range
            0.7-3.5 kb. Library is normalized and enriched for
            full-length clones and was constructed by C. Gruber
            (Invitrogen). Research Genetics tracking code 017. Note:
            this is a NIH_MGC Library."
          Query Match 12.0%; Score 287.8; DB 1; Length 753;
          Best Local Similarity 92.8%; Pred. No. 0;
          Matches 310; Conservative 0; Mismatches 2; Indels 22; Gaps 1;
          QY 1247 GACTGACTTGGAGAAAGCATTTCAGAGTCCTATTTCACCTGGGCTCCAGGTTCTCA 1306
          Db 8 GATTGTACTTGGAGAAAGCATTTCAGAGTCCTATTTCACCTGGGCTCCAGGTTCTCA 67
          QY 1307 GGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTCACAAAGTGGCCCA-- 1364
          Db 68 GGGAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTCACAAAGTGGCCAGT 127
          QY 1365 -----GTTCTCACCTGCTCTGCTCAGCGTCCCAAGGCACTGC 1404
          Db 128 ACACATCTATTTCGATGATGGTTCTCACCTGCTCTGCTCAGCGTCCCAAGGCACTGC 187
          QY 1405 ACAGAAAGCTGAGCTGGAAAGTCCCACTGCTCATCTCTGGGTTTCTGCTCTTTTATT 1464
          Db 188 ACAGAAAGCTGAGCTGGAAAGTCCCACTGCTCATCTCTGGGTTTCTGCTCTTTTATT 247
          QY 1465 TGGTATCCTGTTCTTTTGGCCGTTTCAGTCAATTTGTGCACTCAGCTGAAAGTTGCT 1524
          Db 248 TGGTATCCTGTTCTTTTGGCCGTTTCAGTCAATTTGTGCACTCAGCTGAAAGTTGCT 307
          QY 1525 GCTACTTCTGTCGCTCTGTCGCTGGCGGAGG 1558
          Db 308 GCTACTTCTGTCGCTCTGTCGCTGGCGGAGG 341

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RESULT 19
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 DEFINITION nrhy7-00049-e6 5', mRNA sequence.
 ACCESSION CB783017 GI:29871408
 VERSION CB783017.1
 KEYWORDS Rattus norvegicus (Norway rat)
 SOURCE Rattus norvegicus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 508)
 AUTHORS Angen EST Program.
 TITLE Angen Rat EST Program
 JOURNAL Unpublished (2003)
 COMMENT Contact: Dan Fitzpatrick
 Angen, Inc
 One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00049 row: e column: 6.
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 hypothalamus adult female Wistar rat avg. insert size 2.3
 kb fraction 6 and 7"

Query Match	12.0%;	Score 287.2;	DB 1;	Length 508;
Best Local Similarity	73.6%;	Pred. No. 0;		
Matches 373;	Conservative 0;	Mismatches 88;	Indels 46;	Gaps 1;

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QY      1036 ATAGCACTTGCCTTACGATTCCAAAGACAGCTAGCGAGCCTCTCTATTTCCAGTTGTG 1095
          |||||
DB       2   ATAGCACTGGTGTGCCAATTCCTTAAGAATAATGTAGAGACCTCTATTTCCCAGTTATA 61
          |||||
QY      1096 GAAGGAAGACCATAATCAGAGAGCAGTTTGAGATTTTTTACATTGAATACAGTGCAGCTTAGT 1155
          |||||
DB       62 GAGGGAACAACAGATGAGAGAGCAGCTGAGATTTTACATTTAAACACATTACAGCTTAGC 121
          |||||
QY      1156 AAACCTGTGTCAGAGAAATGTGCCGTATATGAAAAGATCCTGGTGTGGAGCAGTTTAAA 1215
          |||||
DB      122 AAACTATTGCAAGAAAAACATACACGCTTATGAAAAGATCCTGGAATTGAGCAGTTTAAA 181
          |||||
QY      1216 ATGTCAGAAGATTTCATGGGAACCTGGATCAGACTGTACTTTGGAGGAAAAGCAATTCAGAA 1275
          |||||
DB      182 ATGGCAGAAAGGTTGCATGGAACCTGGGTCAAACCTGCACTTGGAGAAACCATTCAGAC 241
          |||||
QY      1276 GTCCCTATTCAA CTTGGGCTCCAAGGTTCTCAGGCAAGTACCTGGAATGCTCTGAAGACGCTG 1335
          |||||
DB      242 ATTCTGCTGGCTTTGGGACCAAACTACTCAGCGAGTACCTGGGTGCCCTCGAACCCCTG 301
          |||||
QY      1336 AGCTTGCTCCTCAGGTGCACAAGTGGCCCA----- 1364
          |||||
DB      302 AGTCAGTCCCTGAGCACACAAGTGGCTCACTAATGACTCTACTAATGGCAGTGGGGACA 361
          |||||
QY      1365 -----GTTCTCACTCCCTGCTCTGCTCAGCGTCCCCACAGGCACCTGCACAGA 1409
          |||||
DB      362 CTCATGGTTTGGAGGTTCTCACTCTGTTCTCCTTAGCACTCCACATGTGCTGTGCAGA 421
          |||||
QY      1410 AAGGCTGAGCTGGAAGTCCCACTGTCATCTCTGGGTTTTCTCTGCTCTTTTATTGTGTT 1458
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DB      422 AAGCTGAACGTGATGTTCCCTGTGTCTCCTGTGTTCTCTGTTCTCTCTCTCTTTTACTTGATA 481
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QY      1470 ATCCTGGTTCTTTTCGGCCGTTTCAGTTC 1496
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DB      482 TTTTGGTTCTTTTCGGCCCAATTATGTC 508
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Db      316  AAGGACAGCAGCTCAAGTGAAGCCATGCTCGTATCAAGGCCCTGATGACAGTAGCATC 375
QY      460  CCTGGCTTTGTGACGCTATCAGGAACCTCAATTCTCTGCACTGCTGGAAGACAGTGTG 519
Db      376  CTTGGATTTATTGATGTTGTAATGATCTAAATTCACGGGAATTAATCTGATGACAAATG 435
QY      520  ATAAGACAAAGCAAGCAGCTGGAAAAGAAATAGTCTTTTATGGAGATGAACCTGGGTT 579
Db      436  ATATGGCAAGGAAGCAAGCTGGAAAAGGAATAGTATTTATGGAGATGATATCTGGATA 495
QY      580  AATATTATCCCAAGCAATTTCTGGAATATGATGAACAACCTCAATTTCTGTGTCAGAT 639
Db      496  AAACTTTTCCCCCAACATTTCTGAATATGATGAACAACCTCAATTTCTGTGTCAGAT 555
QY      640  TACACAGAGTGATTAATATCTCAGGAGCAATTTGGATAAAGTATTAAGAGAGAGAT 699
Db      556  TATACAGAGTGATGAATATGTTACAAGACATTTGATGATATTTTAGAGAGAAATGAC 615
QY      700  TGGGACATATTAAATCC 715
Db      616  TGGGATATGCTATATCC 631

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RESULT 21
CB548333
LOCUS
DEFINITION AMGNNUC:NRHYS-00161-C4-A W Rat hypothalamus (10471) Rattus
CB548333
ACCESSION CB548333.1 GI:29432275
VERSION
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 510)
AUTHORS Angen EST Program.
TITLE Angen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00161 row: C column: 4.
FEATURES
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1..510
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kb fraction 6 and 7"

```

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Query Match 11.0%; Score 263; DB 1; Length 510;
Best Local Similarity 72.9%; Pred. No. 0;
Matches 371; Conservative 0; Mismatches 90; Indels 48; Gaps 3;
QY 1036 ATAGCACTTGGCTTACCGATTCCAAAGACAGTGTAGGAGCCTCTATTTCCAGTTGTG 1095
Db 2 ATAGGACTCGGTTTGCAATTCCTAAGATAATGTAGGAGCCCTTTATTTCCAGTTATA 61
QY 1096 GAAGGAGAACCAATGAGAGACAGTGTAGATTTTACATTTGAATACAGTCAGCTTAGT 1155
Db 62 GAGGAAAAACAGATGAGAGACAGCTGAGATTTTACATTTAAACACATTACAGCTTAGC 121
QY 1156 AAACCTGTTCAGAGAGATGTGCGGTTCATATGA-AAAAGATCTCTGGGTTTGAGCAGTTAA 1214
Db 122 AAACATTTGCAAGAAAAACATACCAGCCTATGATAAAAAGATCTCTGGATTTGAGCAGTTAA 181

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QY 1215 AATGTCAGAAAGATTGATGGAACTGGATCAGACTGTACTTGGAGGAAGACATTTCAGA 1274
Db 182 AATGGCAGAAAGGTTGCATGGAAACTGGGTCAAACTGCACTTTGGAAGAAACCAATTTCAGA 241
QY 1275 AGTCTTATTCAACCTGGGCTCCAAAGTTCTCAGGCAGTACCTGGATGCTCTGAAGACGCT 1334
Db 242 CATCTCTGCTTGGCTTTGGGACCAAAAGTACTCAGGCAGTACCTGGGTGCCCTGAAGACCT 301
QY 1335 GAGCTTGTCCTCGTGAAGTGCACAAAGTGGCTCACTCATCATCTACTCAATGGCAGTGGGAC 1364
Db 302 GAGTCAGTCCCTTGACACACAAAGTGGCTCACTCATCATCTACTCAATGGCAGTGGGAC 361
QY 1365 -----GTTCTCACCTCTGCTCTGCTCAGCGTCCACACAGGCACTGCACAG 1408
Db 362 ACTCATGTTTGGAGGTTCTCACCTCTGTTCTCTTAGCACTCACAATGCTGTGCAG 421
QY 1409 AAGGCTCAGCTGGAAGTCCCACT-GTCACTCTCTGGGTTTCTCTGCTCTTTTATTGG 1467
Db 422 AAGGCTGAACCTGGATGTTCCCTGTTGTCTCTGTTCTCTGCTCTCTTTTACTTGA 481
QY 1468 TGATCCTGTTCTTTTCGGCGCTTCAGGTC 1496
Db 482 TATTTTGGTCTTTTCGGCGAGTCATGTC 510

```

```

RESULT 22
CB765650
LOCUS
DEFINITION AMGNNUC:NRHYS-00390-H6-A W Rat hypothalamus (10471) Rattus
CB765650
ACCESSION CB765650.1 GI:29854041
VERSION
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 418)
AUTHORS Angen EST Program.
TITLE Angen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00390 row: h column: 6.
FEATURES
source
1..418
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrhys-00390-h6"
/note="Vector: pSPORT1; Site 1: Sali; Site 2: NotI; W Rat
hypoThalamus adult female Wistar rat avg. insert size 2.3
kb fraction 6 and 7"

```

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Query Match 10.4%; Score 248.4; DB 1; Length 418;
Best Local Similarity 84.3%; Pred. No. 0;
Matches 279; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 71 TGTCCACGATCGGCTCGGCTCGGACATTTTCGTACCTGTTGCGTAGCGATCAGGTGC 130
Db 87 TGGGCAGATCGGCTCGGCTCGGCGCTTCGTCAGCTCGTAGCGATTGAGGTGA 146
QY 131 TAGGATCGGCTCTCTTCCTCGGGATTTCTCCCGGCTCCCGTCTCTCTGCCAGAG 190
Db 147 TTGGGTCGCGATATTTATTTCGGGATTTCTCCAGCTCTCTGCTGCTCTCTGCCAGAC 206
QY 191 CGGAACACGGAGCGAGCCGCCAGCCCGAACCCTCGGCTGGAGCCAGTTCTTAATGGA 250
Db 207 CGGACATGGTGCAGAGACCCCGAGCCCGAGTCCAGTCTGAACTGA 266

```

align44

Tue Sep 7 08:53:52 2004

Matches 249; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 251 CCAGCTGCCACCACTCTCTTTCAGTAAAGTGTGTTATGTTCTGATAGATCCCTTGAGAG 310
 Db 267 CCAAGTCCGCCACCACTCTTTCAGTAAAGTGTGTTATGTTCTGATAGATCCCTTAAGAG 326
 QY 311 ATGATTTTGTGTTGGTTCAAAGGTTGAAATTTATGCCCTACACAATCTTACCTTGTGG 370
 Db 327 ATGATTTTGTGTTGGTTCAAAGGTTGAAATTTATGCCCTACACAATCTTACCTTGTGG 386
 QY 371 AAAAAGGAGCATCTCACAGTTTGTGGCTGA 401
 Db 387 AAAAAGGAGCGTCTCATAGTTTGTGGCTGA 417

RESULT 23
 AA361388 253 bp mRNA linear EST 21-APR-1997
 LOCUS EST70856 T-cell lymphoma Homo sapiens cDNA 5' end, mRNA sequence.
 DEFINITION
 AA361388
 VERSION
 AA361388.1 GI:2013883
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 253)
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Ene,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.D., Geoghagen,N.S.,
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
 Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
 Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
 Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M. and Venter,J.C.
 TITLE
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 JOURNAL
 Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE
 96026280
 PUBMED
 7566098
 COMMENT
 Other_ESTs: THCT7549
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
 source
 1. .253
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="ATCC (inhost):165712"
 /db_xref="taxon:9606"
 /cell_type="T-lymphocyte"
 /clone_lib="T-cell lymphoma"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI"

Query Match 9.9%; Score 237.9; DB 1; Length 253;
 Best Local Similarity 98.0%; Pred. No. 0;

RESULT 24
 CD516167
 LOCUS
 DEFINITION
 AGENCOURT 14372444 NIH_MGC 181 Homo sapiens cDNA clone
 IMAGE:30397569 5', mRNA sequence.
 CD516167
 VERSION
 CD516167.1 GI:31447885
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 976)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 COMMENT
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein
 CDNA Library Preparation: Invitrogen Corp
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDMA481 row: b column: 10
 High quality sequence start: 24
 High quality sequence stop: 415.

FEATURES
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 1. .976
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="NIH_MGC 181"
 /dev_stage="Unknown"
 /lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
 /note="Vector: PCMV-SPOK6.1; Site_1: NotI; Site_2: EcoRV
 (destroyed); Library is oligo-dT primed and directionally
 cloned (EcoRV site is destroyed upon cloning). Average
 insert size 1.42 kb. Library was constructed by
 (Invitrogen). Note: this is a NIH_MGC Library."

Query Match 9.6%; Score 229; DB 1; Length 976;
 Best Local Similarity 83.9%; Pred. No. 0;
 Matches 265; Conservative 0; Mismatches 5; Indels 46; Gaps 1;

```

QY 1289 TGGGCTCAAGTTCTCAGGAGTACCTGGATGCTCTGAAGACGCTGAGCTTGCCTGA 1348
Db 10 TCGGATCAAGGTTCTCAGGAGTACCTGGATGCTCTGAAGACGCTGAGCTTGCCTGA 69
QY 1349 GTGCACAAAGTGGGCCA-----1364
Db 70 GTGCACAAAGTGGGCCAAGTACGACATCTATTTCGATGCTGGGAGCTGCTGGTTTGG 129
QY 1365 --GTTCTCACCTGCTCTCTCAGCTCCACAGGCACTGCACAGAAAGGCTGAGCTGG 1422
Db 130 AGGTTCTCACCTGCTCTCTCAGCTCCACAGGCACTGCACAGAAAGGCTGAGCTGG 189
QY 1423 AAGTCCAGTCACTCTCTCTGGGTTTCTCTGCTCTTTATTATTTGGTGATCTCTGTTT 1482
Db 190 AAGTCCAGTCACTCTCTCTGGGTTTCTCTGCTCTTTATTATTTGGTGATCTCTGTTT 249
QY 1483 CGGCGCTTCACGTCATTGTGTGCACTCAGCTGAAAGTTGCTGCTACTTCTGTGGCTCT 1542
Db 250 CGGCGCTTCACGTCATTGTGTGCACTCAGCTGAAAGTTGCTGCTACTTCTGTGGCTCT 309
QY 1543 CTGGCTGGCGGAGG 1558
Db 310 CTGGCTGGCGGAGG 325

RESULT 25
T32542 253 bp mRNA linear EST 06-SEP-1995
LOCUS EST50552 Human Gall bladder Homo sapiens cDNA 5' end similar to
DEFINITION None, mRNA sequence.
ACCESSION T32542
VERSION T32542.1 GI:614640
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 253)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,
Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geohagen,N.S.M.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,J.P.S.,
Kelley,J.M., Klieck,K.M., Kelley,J.C., Liu,L.-J., Marmaros,S.M.,
Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,
Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,
Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,
Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
JOURNAL Nature 377, 3-174 (1995)
MEDLINE 96026280
PUBMED 7566098
COMMENT Other ESTs: THCL15950
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse
Location/Qualifiers

```

```

source 1. .253
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):103110"
/db_xref="taxon:9606"
/clone_lib="Human Gall bladder"
/notes="Organ: gallbladder"

Query Match 9.1%; Score 217.4; DB 1; Length 253;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 242; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY 11 GAAGCGCGGCTGCAGCAGGCGGAGGCTCCAGGTGGGTCGGTTCCGATCCAGCCTAGCG 70
Db 2 GGAAGCGCGGCTGCAGCAGGCGGAGGCTCCAGGTGGGTCGGTTCCGATCCAGCCTAGCG 61
QY 71 TGTCACAGATGCGGCTGGGCTCCGGACTTTGCTACTGTTGCGTAGCGATCGAGTGC 130
Db 62 TGTCGCNATGCGGCTGGGCTCCGGACTTTGCTACTGTTGCGTA-NGATCGAGTGC 120
QY 131 TAGGGATCGCGTCTCTTCGGGATTTCTTCCGGCTCCCGTTCCTCTGCCAGAG 190
Db 121 TAGGGATCGCGTCTCTTCCTTCGGGATTTCTTCCGGCTCCCGTTCCTCTGCCAGAG 180
QY 191 CGGAACAGCGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 250
Db 181 CGGAACAGCGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 239
QY 251 CCACGCTGCCACCA 264
Db 240 CCACGTTGCCACCA 253

RESULT 26
BF791461 1205 bp mRNA linear EST 12-JAN-2001
LOCUS 602251501P1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4343713 5',
DEFINITION mRNA sequence.
ACCESSION BF791461
VERSION BF791461.1 GI:12096515
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1205)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-k@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: Incyte Genomics, Inc.
found through the I.M.A.G.E. Consortium information can be
http://image.llnl.gov
Plate: LLAN9961 row: b column: 02
High quality sequence stop: 328.
Location/Qualifiers
1. .1205
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4343713"
/lab host="adrenal cortex carcinoma, cell line"
/clone_lib="NIH MGC_84"
/notes="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
Noti; Site_2: SalI; Cloned unidirectionally; oligo-dr_1:
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.

```

```

/db xref="taxon:9606"
/dev stage="Adult"
/clone lib="AN0094"
/notes="Organ: amnion normal; Vector: puc18; Site: 1: SmaI;
Site: 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

Query Match      8.6%; Score 206.2; DB 1; Length 350;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 208; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 985 ATCCGACATCCAAAGCAGCTCCATAGACGATGGCTGGACACACTGGCGATAGCATT 1044
Db 350 ATCCGACATCCAAAGCAGCTCCAAAGCAGCTGGCTGGACACACTGGCGATAGCATT 291

QY 1045 GCGTTACCGATTCCAAAAGACAGTGTAGGAGCCCTCTATTCCCGAGTTGTGGAAGAGA 1104
Db 290 GCGTTACCGATTCCAAAAGACAGTGTAGGAGCCCTCTATTCCCGAGTTGTGGAAGAGA 231

QY 1105 CCAATGAGAGAGCAGTTCAGATTTTACATTTGAATACAGTGCAGCTTAGTAACTGTG 1164
Db 230 CCAATGAGAGAGCAGTTCAGATTTTGAATACAGTGCAGCTTAGTAACTGTG 171

QY 1165 CAAGAGATGTCCCGTCATATGAAAAAGATC 1195
Db 170 CAAGAGATGTCCCGTCATATGAAAAAGATC 140

```

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RESULT 28
LOCUS      244206      318 bp      mRNA      linear      EST 14-NOV-1994
DEFINITION HSC1VA011 normalized infant brain cDNA Homo sapiens CDNA clone
c-1va01, mRNA sequence.
ACCESSION 244206
VERSION   244206.1 GI:573331
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 318)
AUTHORS  Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,
Devignes, M.D., Duprat, S., Houllatte, R., Jumeau, M.N., Lamy, B.,
Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,
Sebatiani-Kabatchis, C. and Tessier, A.
TITLE     IWAGE: molecular integration of the analysis of the human genome
and its expression
JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE   95277534
PUBMED    7757816
COMMENT   Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1 rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress library idt: C; Genexpress_sequence_idt: ylc-1va01
Seq primer: (-21)M13 universal.
FEATURES  Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="c-1va01"
            /sex="Female"
            /tissue_type="total brain"
            /dev_stage="3 months old"

```

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Note: this is a NIH_MGC Library."

Query Match      8.8%; Score 211; DB 1; Length 1205;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 308; Conservative 0; Mismatches 35; Indels 12; Gaps 7;

QY 783 GCTCAGGAGATGACAGCGTGTGATGAAGATCCACACC-TCACTGAGTCGGAAGAGA 841
Db 1 GCTGAGCGAGATGACAGCGTGTGATGAAGATCCACACCCTCACTGCGAGTGAAGAGA 60

QY 842 GAGAGACGCCCTTTACCAATTTGCTGGTCTTTTGGTGACATGCGCATCTGAACAG 901
Db 61 GAGAGACGCCCTTTACCAATTTGCTGGTCTTTTGGTGACATGCGCATCTGAACAG 120

QY 902 GAAGTCACGGGCGCTCC-TCCACCGAGGAGGTGAATACA-----CCTCTGATTTTAATCAG 956
Db 121 GAAGTCACGGGCGCTCCATCCACCGAGGAGGTGAATACAGCCTCTGATTTTAATCAGAT 180

QY 957 TTCTCGGTTTGAAGAAACCCGGTGATATCCGATCCAAAGACG-TCCAAATGAGCGG 1015
Db 181 TACTCGGTTTGAAGAAACCCGGTGATATCCGATCCAAAGACGATCCAAAGACGCG 240

QY 1016 ATGTGGC---TCCGACACTGGGATAGCACTTGGCTTACCGA-TTCCAAAACACAGTGA 1071
Db 241 ATGTGGCATGCCACATGACGATAGCACTTGGATTTACCGAGTTCCAAAACACAGTGA 300

QY 1072 GGAGC-CTCCATTCCCGAGTTGTGAAGGAAGACCAATGAGAGCAGCTTGAGA 1125
Db 301 GGAGCAGCTCTTATTTCCCGAGTTGTGAAGGAAGACCAACTGAGCAGACAGAAA 355

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```

RESULT 27
LOCUS      BQ293001/c      350 bp      mRNA      linear      EST 15-MAY-2002
DEFINITION PM1-AN0094-240800-002-d02 AN0094 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ293001
VERSION   BQ293001.1 GI:20801951
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 350)
AUTHORS  Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Garvalho, A.F., Mateukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., Gooliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20202863
PUBMED    10737800
COMMENT   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-AN0094-
240800-002-d02&t3=2000-08-24&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 350.
FEATURES  Location/Qualifiers
           1..350
            /organism="Homo sapiens"
            /mol_type="mRNA"

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/clone_lib="normalized infant brain cdna"
 /note="Organ: brain; Vector: lafmid BA; Site:1: HindIII;
 Site 2: NotI; sex=Female; dev stage=3 months old;
 isolate=muscular atrophy patient; tissue type=total
 brain; total mRNA was oligo-(dT) primed and directionally
 cloned 5' -> 3' into the HindIII -> NotI sites of the
 lafmid BA vector. Clone library from B.Soures, Psychiatry
 Dept. Columbia University, USA. Normalization_method:
 Bento Soares, P.N.A.S in press"

Query Match 8.6%; Score 205; DB 1; Length 318;
 Best Local Similarity 98.3%; Pred. No. 0;
 Matches 226; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 QY 4 GGAGCCGGAAGCGCGCTCCAGCAGCGGCGAGGCTCCAGGTGGGTGGTTCGGCATCCAG 63
 Db 1 GGAGCCGGAAGCGCGCTCCAGCAGCGGCGAGGCTCCAGGTGGGTGGTTCGGCATCCAG 60
 QY 64 CTTAGCGGTTCACGATGCGGTGGCTCCGGGACTTTTCGCTACCTGTTGCGTAGCGATC 123
 Db 61 CTTAGCGGTTCACGATGCGGTGGCTCCGGGACTTTTCGCTACCTGTTGCGTAG-GATC 119
 QY 124 GAGGTGCTAGGATCGCGGTCTTCCTTCGGGGATTCCTCCGGCTCCCGTTCGTTCCCT 183
 Db 120 GAGGTGCTAGGATCGCGGTCTTCCTTCGGGGATTCCTCCGGTCCCGTTCGTTCCCT 179
 QY 184 GCCAGAGCGGAACACGAGCGGAGCGCCGCCAGCGCCGGAACCTCGGCTGG 233
 Db 180 GCCAGAGCGGAACACGAGCGGA-NCCGAGCGCCCGAACCCTCGGCTGG 228

RESULT 29
 BG923173
 LOCUS
 DEFINITION 602824014F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4952955 5',
 mRNA sequence.

BG923173.1 GI:14303649

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: Incyte Genomics, Inc.
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLAM10911 row: k column: 04
 High quality sequence stop: 683.
 Location/Qualifiers

FEATURES
 source

1. 806
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4952955"
 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Mam6"
 /note="Organ: mammary; Vector: pCMV-SORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator

providing samples: Jeffrey Green, M.D., NIH"

Query Match 8.4%; Score 200; DB 1; Length 806;
 Best Local Similarity 71.0%; Pred. No. 0;
 Matches 272; Conservative 0; Mismatches 65; Indels 46; Gaps 1;

QY 1222 GAAAGATTGATGGGAATCGGATCAGACTGTACTTGGAGGAAAGATTGAGAGTCCTTA 1281
 Db 1 GAAAGATTGATGGGAATCGGATCAGACTGTACTTGGAGGAAAGATTGAGACATTCG 60
 QY 1282 TTCAACCTGGGTCCAGGTTCTCAGGCACTACCTGGATGCTCTGAAGACGCTGACCTG 1341
 Db 61 CTTGGCTGGGACCAAGTACTCAGGCATTACCTGGGTGCCCTGAAGACCTGAGTCTG 120
 QY 1342 TCCCTGAGTGACAAAGTGGCCCA----- 1364
 Db 121 TCCCTGAGCACAAAGTGGCTCAATATGACATGTACTCCATGGCAGTGGGAACACTCATA 180
 QY 1365 -----GTTCCTCACCTGCTCCTGCTCAGCGTCCACAGGCACTGCACAGAAAGGT 1415
 Db 181 GTTTTGGAGGTTCGCGCTGTTCTCTTAGCACTCCACATGTGCTGTGCAGAAAGGT 240
 QY 1416 GAGCTGGAAGTCCCACTGTGATCTCCTGGGTTTCTCTGCTCTTTTATTGGTGATCTCTG 1475
 Db 241 GAGCTGGAATGTTCTCTGTTGGCTGTGTTTGGCTGCTTTTACTTGGTGTGTTTG 300
 QY 1476 GTTCTTTCGGCGGTTTCAGTCAATTGTGTGCACTCAGCTGAAAGTTCGTCTACTTCTGT 1535
 Db 301 GTTCTTTCGGCAATTCATGCTCGGTGTGCACTCATCTGAGAGTCGTGCTACTCTGT 360
 QY 1536 GGCTCTCTGCTGGCTGGCGGAGG 1558
 Db 361 AGCTCTCTGCTGGCTGGAGTGG 383

RESULT 30

BC051059
 LOCUS
 DEFINITION Mus musculus mRNA similar to hypothetical protein FLJ20265 (cdna
 clone IMAGE:5010465).

ACCESSION
 VERSION
 KEYWORDS
 SOURCE

BC051059.1 GI:30047881

HTC.

Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3150)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,

Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL

22388257

PUBMED

REFERENCE

2 (bases 1 to 3150)

Strausberg, R.

TITLE	Direct Submission
JOURNAL	Submitted (11-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgabps-remail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nhgri.nih.gov Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Young, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L., H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 108 Row: f Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
analysis has the following problem: frame shifted.

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analysis
This clone has the following problem: frame shifted.
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old mouse. Taken by biopsy."
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source

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Best Local Similarity	71.0%;	Prod. No. 0;		
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QY	1222	GAAGATTGCATGGGAAC	TGGACTGACACTGCTACTCTGGAGGAAAGCA	TTCCAGAAGTCCTA 1281
DB	1	GAAGAATTACATGGAAAC	TGGGTCCTAACTGCACCTGGAGGAAACCA	TTCCAGACATTCG 60
QY	1282	TTTCAACCTGGGCTCC	AAAGTTTCCAGGAGTACCTGGATGCTCTGAAGACGCT	GAGCTTG 1341
DB	61	CTTGGCCTGGGACCA	AAAGTACTCAGGCATTACCTGGTGCCCTGAAGACCC	TGAGTCTG 120
QY	1342	TCCTGAGTGCACAAGT	GGCCCCA-----	----- 1364
DB	121	TCCTTGAGCACACAAG	TGGCTCAATATGACATGTACTCCATGGCAGTGGG	NACACTCATA 180
QY	1365	-----	GTTCACACCTGCTCCTGCTCAGCGTCCCA	CAGGCATGCAACAGAAAGCT 1415
DB	181	GTTTTCGAGGTTCTCG	CCCTGTCTCCTTAGCACTCCACATGTGCTGTG	CAGAAAGGCT 240
QY	1416	GAGCTGGAAGTCCCACT	GTGCATCTCTGGGTTTTCTCTGCTCTTTATT	TTCGGTGATCCTG 1475
DB	241	GAGCTGGAATGTTCT	CTGTGTTCGCTGTGTGTTTTCGCTGCTCTTT	TACTTGGTGTTTG 300
QY	1476	GTTCCTTCGGCGGTT	TCAGCTCATTTGTCGCACTCAGCTGAAAGT	TCGTGCTACTTCTGT 1535
DB	301	GTTCCTTCGGCGAAT	CATGTCCCTGGTGTGCACTCATCTGAGAGCT	CGTGCTACCTCTGT 360

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QY      1536  GGCTCTCTGCTGGCGGCAGG 1558
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Db      361  AGCCTCTCGTGGCTGCAGTGG 383
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RESULT 31
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AGENCOURT_6405774 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5500197
5', mRNA sequence.
ACCESSION      BM455257
VERSION        BM455257.1 GI:18504285
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1099)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM12134 row: 1 column: 22
High quality sequence stop: 673.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_85"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life technologies.
Note: this is a NIH MGC Library."

FEATURES
source

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	Query Match	8.3%;	Score 199;	DB 1;	Length 1099;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
	Matches 199;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	35	GCTCCAGGTGGGTTCGGTTCCGGCATCCAGCCTAGCGTGTCCACGATGCGGTGGGCTCGG	94			
Db	1	GCTCCAGGTGGGTTCGGTTCCGGCATCCAGCCTAGCGTGTCCACGATGCGGTGGGCTCGG	60			
Qy	95	GGACTTTTCGTACTCTTTGGGTAGCGATCGAGGTCTAGGATCGCGGTCTCCTTCGCG	154			
Db	61	GGACTTTTCGTACTCTTTGGGTAGCGATCGAGGTCTAGGATCGCGGTCTCCTTCGCG	120			
Qy	155	GATTCCTCCGGTCCGGTTTCGTTCTCTCCAGAGCGGAACACAGAGCGGAGCCCCAG	214			
Db	121	GATTCCTCCGGTCCGGTTTCGTTCTCTCCAGAGCGGAACACAGAGCGGAGCCCCAG	180			
Qy	215	CGCCCGAACCTCGGCTGG	233			
Db	181	CGCCCGAACCTCGGCTGG	199			

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RESULT 32
BG389289
LOCUS
DEFINITION
      BG389289          789 bp      mRNA      linear      EST 12-MAR-2001
      602413937F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4522449 5',
      tRNA sequence.

```

Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
 Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Mackesich, D.,
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
 Sparks, M.J., Van Slichtenhorst, I., Vogel, P., Walke, W., Xu, N.,
 Zhu, Q., Person, C. and Sands, A.I.
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 Contact: Zambrowicz BP
 OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.
 Location/Qualifiers
 source 1..501
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 /clone="OST248759"
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 Best Local Similarity 57.3%; Pred. No. 0;
 Matches 398; Conservative 0; Mismatches 79; Indels 217; Gaps 6;
 QY 232 GGAGCCAGTTCTAACTGGACACAGCTGCCACCACTCTCTTCAGTAAAGTTGTTATTGTT 291
 Db |||||
 QY 3 GGAGTCGGTTCGAACTGGACCAAGCTGCC-CCACCTCTCTTCAGTAAAGTTGTTATTG 61
 Db |||||
 QY 292 CTGATAGATGCGCTTGAGAGATGATTTTGTGTTGGGTCAAAGGTGTGAATTTATGCCC 351
 Db |||||
 QY 62 TTGATAGATGCAATTAAGAGATGATTTTGTGTTGGGTGAAAGGTGTGAAGTATATGCCC 121
 Db |||||
 QY 352 TACACAACCTTACCTTTGTGAAAAAGGAGCATCTCACAGTTTGTGGCTCAAGCAAGCA 411
 Db |||||
 QY 122 TACACAACGTATCTGGTAGAAAAGGAGCATCTCATAGCTTTGTGGCTGAGGCAAGCA 181
 Db |||||
 QY 412 CCTACAGTTACTATGAGCTCGAATCAAGGCAATGATGACGGGAGAGCCTTCCTGGCTTGTG 471
 Db |||||
 QY 182 CCCACAGTTACTATGCTCGAATCA----- 206
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 QY 472 GAGGTCAATCAGGAACCTCAATTCCTCGTCACTGCTGGAAGACAGTGTGATAAGACAAGCA 531
 Db |||||
 QY 207 ----- 206
 QY 532 AAAGCAGCTGAAAAAAGAAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTTATCCCA 591
 Db |||||
 QY 207 ----- 206
 QY 592 AAGCATTTTGTGCAATGATGGAACAACCTCAATTTTCTGTCTCAGATTACACAGAGGTG 651
 Db |||||
 QY 207 -----AGGTG 211
 QY 652 GATAATAATGTCAAGGCAATTTGGATAAGTATTAAAAAGAGGAGATTGGACATATTA 711
 Db |||||
 QY 212 GATAAATATGTCAAGGCAATTTGGACAAAGTATTAAAAAGAGGAGACTGGGATGTGTTA 271
 Db |||||
 QY 712 ATCTCCCTACCTGGGGCTGGACACACATTTGGCCACATTTCAAGGSCCAACAGACCCCTGT 771
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 QY 272 ATCTTTCATCTATAGGACTGGATCACAATTTGCCACATTTCTGGGCCCAACAGCCCCCTG 331
 Db |||||
 QY 772 ATTGGCGAGAGCT--GAGCGAGATGGACAGCGTGTGATGAAGATCCACACTCACTGCA 830
 Db |||||
 QY 332 ATTGGTCAAGACTCTNGCNAATGGACAGTNGCTGATGAATGAATCCNCCCTTCACTGCT 391
 Db |||||
 QY 831 GT--CGAAGGAGAGAGACGCCCTTTACCCAATTTGCTGGTTCT--TTGTGGTGACCAATGG 887
 Db |||||
 QY 392 GNTCGAAAGGACTGAAGACTCTCTTACCCAGTNGCTGNTCTCNNGTNGCGACCAATGG 451
 Db |||||

888 CAT-~~GTCTGAACACGAGTACACGGGCTCT~~ 919
 DB AANTGNCCTGNAACTGCNAGCCTGGCNCCTCT 485

RESULT 34
 BI051441/c 318 bp mRNA linear EST 15-JUN-2001
 LOCUS CM4-GN0332-120101-653-g04 GN0332 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION BI051441
 VERSION BI051441.1 GI:14458971
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 318)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-GN0332-120101-653-g04&t3=2001-01-12&t4=1>)
 Seq primer: puc 18 forward
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 High quality sequence stop: 318.
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 /dev_stage="Adult"
 /clone_lib="GN0332"
 /note="Organ: placenta normal; Vector: puc18; Site: 1;
 Sma1; Site 2: Sma1; A mini-library was made by cloning
 products derived from ORESTES PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer
 Research) profiles into the puc 18 vector. Reverse
 transcription of tissue mRNA and cDNA amplification were
 performed under low stringency conditions."

Query Match 7.7%; Score 184.5; DB 1; Length 318;
 Best Local Similarity 94.8%; Pred. No. 0;
 Matches 201; Conservative 0; Mismatches 10; Indels 1; Gaps 1

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 DB 212 GGTGATATCCGACATCCAAAGCAGCTCCAAATAGACGGATGTGGCTCGACACTGGCGATA 153
 QY 1039 GCACCTGGCTTACCGATTCCA-AAACACAGTGTAGGAGCCTCTATTCCACAGTTGTGGA 109
 DB 152 GCACCTGGCTTACCGATTCCATTAACACAGTGTAGGAGCCTCTATTCCACAGTTGTGGA 93
 QY 1098 AGGAAGACCAATGAGAGAGCAGTTGAGATTTTTCATTTGATATACAGTCAGCTTAGTAA 115

QY 1365 -GTTCTCACCTGCTCTCTGCTCAGCTCCACAGGCACTCCACAGAAAGGCTGAGCTGGA 1423
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 Db 241 GGTTTTGTCTGCTACTTTTCTCAGCGTGCACAAAGAGCTCTGAGCAGTGGGCGCAAAATTGA 300
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 QY 1424 AGTCCCACTGTCATCTCCTGGGTTTCTCGCTCTTTTATTGGTGATCTGGTTCCTTC 1483
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 Db 301 AGTGCCCTCTCCCTCCGCTCTCTCTCTGCTGTTTACTTGATGTGCTGATGCTGTG 360
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 Db 421 NNNNNNACAGCAG 434
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RESULT 36

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 LOCUS RC1-BT0254-071100-118-h03 BT0254 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION BF746141
 VERSION BF746141.1 GI:12072817
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 355)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BT0254-
 071100-118-h03&t3=2000-11-07&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 355.

FEATURES

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 /note="Organ: breast; Vector: puc18; Site: 1; SmaI; Site 2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

Query Match 7.2%; Score 172.6; DB 1; Length 355;
 Best Local Similarity 88.6%; Pred. No. 0;
 Matches 187; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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 QY 1797 CCCCACTGAGGGGTGTGTAATCGGACAGCTCCACAGAGGTGTGGAGCTCAG 1856
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 Db 205 CCCCGGCTGAGGGGTGTGTAATCGGACAGCTCCACAGAGGTGTGGAGCTCAG 264
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 QY 1857 CTGAGGGAAGAGACAATCGCCCTGGACACTCAGAGAGGTCAAAGGAGACTTGGTCG 1916
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 Db 265 CTGAGGGAAGAGACAATCGCCCTGGACACTCAGAGAGGTCAAAGGAGACTTGGTCG 324
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 QY 1917 CACCACTCATCTGCGCCACCCCGCAGATGCAT 1947
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RESULT 37

BI026475/c
 LOCUS CM4-MT0286-070201-749-b12 MT0286 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION BI026475
 VERSION BI026475.1 GI:14433105
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 264)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-MT0286-
 070201-749-b12&t3=2001-02-07&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 6
 High quality sequence stop: 264.

FEATURES

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 /dev_stage="Adult"
 /clone_lib="MT0286"
 /note="Organ: narrow; Vector: puc18; Site: 1; SmaI; Site 2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

Query Match 6.9%; Score 165.2; DB 1; Length 264;
 Best Local Similarity 98.2%; Pred. No. 0;
 Matches 167; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

align44

Tue Sep 7 08:53:52 2004

QY	1030	CTGGCGATAGACCTGGCTTACCGATCTCCAAAGACAGCTAGTAGGAGCGCTCTATTCCCA	1089
Db	264	CTGGCGATAGACCTGGCTTACCGATCTCCAAAGACAGCTAGTAGGAGCGCTCTATTCCCA	205
QY	1090	GTTGTGAAGGAGACCAATGAGAGAGCAGTGTGAGATTTTACATTTGAATACAGTGCAG	1149
Db	204	GTTGTGAAGGAGACCAATGAGAGAGCAGTGTGAGATTTTACATTTGAATACAGTGCAG	145
QY	1150	CTTAGTAACCTGTTGCAAGAGATGTGCGCTCATATGAAAAGATCCCTGG	1199
Db	144	CTTAGTAACCTGTTGCAAGAGATGTGCGCTCATATGAAAAGATCCCTGG	95
RESULT 38			
LOCUS	BX077539	764 bp	linear
DEFINITION	BX077539 AGENAE Rainbow trout normalized multi-tissues library (tcad) Oncorhynchus mykiss cdna clone tcad0004a.m.24 5prim, mRNA sequence.	EST 25-APR-2003	
ACCESSION	BX077539	1	GI:27740958
VERSION	BX077539		
KEYWORDS	Oncorhynchus mykiss (rainbow trout)		
SOURCE	Oncorhynchus mykiss		
ORGANISM	Oncorhynchus mykiss		
REFERENCE	Govoroun, M., Guiguen, Y. and Le Gac, F.		
AUTHORS	Construction and primary characterization of normalized cdna libraries in rainbow trout, Oncorhynchus mykiss		
TITLE	Unpublished (2003)		
JOURNAL	Contact: Guiguen Y		
COMMENT	INRA - SCRIBE Campus de Beaulieu, RENNES cedex, 35042, France Tel: 02.23.48.50.09 Fax: 02.23.48.50.20 Email: Yann.Guiguen@beaulieu.rennes.inra.fr Sequence cleaned of vector, adaptor and repetitions. Contact us at signasupport@jouy.inra.fr to obtain the chromatogram of this sequence. Plate: 0004 row: m column: 24 Seq primer: T7.		
FEATURES	source		
	1..764		
	/organism="Oncorhynchus mykiss"		
	/mol_type="mRNA"		
	/db_xref="taxon:8022"		
	/clone="tcad0004a.m.24"		
	/tissue_type="adipose tissue, blood, brain, differentiating gonads, interrenal, intestine, liver, muscle, ovary, pituitary, testis"		
	/dev_stage="unknown"		
	/lab_host="DH10B"		
	/clone_lib="AGENAE Rainbow trout normalized multi-tissues library (tcad)"		
	/note="Vector: pT7T3D-pac; Clone distribution: AGENAE Resource centre. Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, France"		
Query Match	6.8%	Score 163.4;	DB 1; Length 764;
Best Local Similarity	60.4%	Pred. No. 0;	
Matches 269;	Conservative	0; Mismatches 176;	Indels 0; Gaps 0;
QY	70	GTGTCACAGATCGGCTCGGAGCTTCGCTACCTGTCGCTAGCAGTCGAGTG	129
Db	251	GTGTCACAGATCGGCTCGGAGCTTCGCTACCTGTCGCTAGCAGTCGAGTG	310
QY	130	CTAGGATCGGCTTCCTTCGCGGATTCCTCCCGCTCCCGCTTCCTCTGCGAGA	189
Db	311	TTAGGATCGGCTTCCTTCGCGGATTCCTCCCGCTTCCTCTGCGAGA	370
QY	190	CGGAAACACGAGCGGAGCCGCCAGCCCTCGGCTGGAGCAGCTTCTTAACCTGG	249
Db	371	TCGAAAGACAGCTTGTTCAGATGTTCCGCTGAACTTACCGAAGATCCCTCACTCC	430
QY	250	ACCACGCTGCCACCACTCTCTTCAGTAAAGTGTGTTATGTTGTGATGATGCTCTCAGG	309
Db	431	TCCAAAGTCCCGAGCGCCCTTTCAAGAGAGTAGTGTGATGATGCTCTCAGG	490
QY	310	GATGATTTTGTGTTGGTCAAGGGTGTGAATTTATGCTCTACACAACTTACCTTGTG	369
Db	491	GAGGACTTTGTGTTGGTCCAAATGGGAGAAATACATGCTTACATCAGGACCTTGGT	550
QY	370	GAAAAGGAGCATCTCACAGTTTGTGCTGAAGCAAGCCACCTTACTATGCTCT	429
Db	551	GAGAGGGGCTCACATACAGCTTGTGTCGAAGCAAGCCCTTACTATGCTCT	610
QY	430	GGAATCAAGGATTCATGACGGGGAGCTTCTGCTGTTGTCAGTCTATCAGGACCTC	489
Db	611	AGAATCAAGGCTTACACAGTAGTATCCCGGCTTCATCGAGTGTGATGACCTG	670
QY	490	AATTCCTCTGCACTGCTGGAAGACA	514
Db	671	AACTCCCGAGCGCTGCTGAGGACA	695
RESULT 39			
LOCUS	AA356939	252 bp	mRNA
DEFINITION	EST65571 Jurkat T-cells III Homo sapiens cdna 5' end, mRNA sequence.	linear	EST 21-APR-1997
ACCESSION	AA356939	1	GI:2009258
VERSION	AA356939		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 252)		
	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hung, J., Li, H., Meisner, P.S., Olsen, H., Raymond, P.J., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Hasseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.		
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence		
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)		
MEDLINE	96026280		
PUBMED	7566098		
COMMENT	Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Fax: 3018699056 Email: arkerlav@tigr.org For clone availability, please check the TIGR Human Gene information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tldb/hgi/hgi.html) Seq primer: M13 Reverse.		

Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France"

Query Match 6.6%; Score 158.2; DB 1; Length 744;
Best Local Similarity 56.8%; Fred.No. 0;
Matches 301; Conservative 0; Mismatches 183; Indels 46; Gaps

QY 1064 ACAGTGTGGGAGCCTCCTATTCCAGTTGTGGAGGAACCAATCAGAGAGCAGTTGA 11
| | | | |
Db 740 ACAGCGTGCGGCAGACTCATCAGCCCCTGTTGACGAGGCCCTCGCTCAGGAGCACAGTCG 69
| | | | |
QY 1124 GATTTTTACATTGTAATACAGTGCAGCTTAGTAACTGTTGCAAGAGAATGTCCCGTCAT 11
| | | | |
Db 680 GCTTTCTCAGCTCAAGCGCCACCAGCTGAGCTACCTGCTGAAGGACAGCATGCCAGCCT 62
| | | | |
QY 1184 ATGAAAAGATCCTGGGTTTTGACGAGTTTAAATGTCAGAAAGATTGCATGGGAACTGGA 12
| | | | |
Db 620 ATGAGAAAGAGAGGGCTATGAGCAGTTCCGTTGGCAGAGAACTCCCATGTTAATCTGG 56
| | | | |
QY 1244 TCAGACTGTACTTGGAGGAAAAGCATTCAGAAGTCTCTATTACACTGGGCTCCAAGTTC 13
| | | | |
Db 560 TGAAGCTAGTGGTGGAGGGCAAACATCAGAGGTGCTGACCAACATGGGGAAGAAGTGT 50
| | | | |
QY 1304 TCAGCAGTACTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGG-- 13
| | | | |
Db 500 TCAAGCAGTACTGGAGGCCCTCAGGGCCATGAGTGAAGCCCTCAGCAAGAGCTGGGCA 44
| | | | |
QY 1361 -----CCCCAGTTCTCACCTGC 13
| | | | |
Db 440 AATATGACATAATTCATGGTGGGATGGTCTCTTGTCTTCAGCTCTCTCTCTCC 38
| | | | |
QY 1378 TCTGTCTCAGCGTCCACAGGCACTGCACAGAAAGCGCTGAGCTGGAAGTCCCATGTGAT 14
| | | | |
Db 380 TGCTGTGGCCATGCCCGAGGACACTGAGCAGTGCCTCAGAGGTGATCTCCCTGTGTCT 32
| | | | |
QY 1438 CTCTGGGTTTTCTGTGCTCTTTTATTTTGGTGATCTGTTCTTTTCGGSCGCTTCAAGTCA 14
| | | | |
Db 320 CTGCTCTGTCTCGCTGCCCTCTACCTGCTCTGTTGCTCTCTCTCCGTGGCACGTGC 26
| | | | |
QY 1498 TTGTGTGACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGG 15
| | | | |
Db 260 TGTGTGACCTCGGCCGAGAGCTCCTGTTACTTCTGCAGCCTCTCTCTCG 21
| | | | |

RESULT 41
BU130677
LOCUS 603116501F1 CSEQCHL21 Gallus gallus mRNA linear EST 25-NOV-2000
DEFINITION sequence.
ACCESSION BU130677
VERSION BU130677.1 GI:25342596
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 739)
Boardman,P.E., Sans-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.F.,
Pong,W.T., Rickie,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel.: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMLN at:
<http://image.llnl.gov>
 Plate: LLM11058 row: g column: 10
 High quality sequence start: 15
 High quality sequence stop: 584.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N-3"
 /db_xref="taxon:10090"
 /clone="IMAGE:5010465"
 /tissue_type="tumor, biopsy sample"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Mam2"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Salt; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

FEATURES
 source
 1..739
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
 /clone="ChEST71b2"
 /dev_stage="36"
 /lab_host="DH10B"
 /clone_lib="CSECHL21"
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 [5'ggccgctgcagcccgatccgaaataaaag]
 [5'aattcttttccggtatccgggctgcagc]

Query Match 5.1%; Score 123; DB 1; Length 758;
 Best Local Similarity 66.4%; Pred. No. 0;
 Matches 241; Conservative 0; Mismatches 70; Indels 52; Gaps 5;
 1256 TGGAGGAAAGCATT-CAGAACTCTATTCAACCTGGGCTCCAAAGTTCTCAGGCGATAC 1314
 50 TGGAGGAAATATCTTGCAGACATTCCTTGGCTGGGACCAAGTACTCAGGCATTAC 109
 1315 C-TGGATGCTCTGAGAGCGTGTGCTCCCTGAGTGCACAAAGTGCCCCA----- 1364
 110 CGTGGTGGCCCTGAAGACCCCTGAGTCTGCTCCTGAGCACACAAAGTGGCTCAATATGACAT 169
 1365 -----GTTCTCACCTGCTCCTGCTCAG 1387
 170 GTACTCCATGGCAGTGGGAACACTATAGTATTTGGAGGTTCTCGCCCTGTTCTCCTTAG 229
 1388 GGTCCCAAGCAGCCTGACAGAAAGCGTGTGAGTGGAGTCCCACTGTCTCATCTCTGCG--G 1445
 230 CACTCCACATGTGCTGTGTCAGAAAGGTGAGTGTGATGTTCTCTGATAGTGGCTGTATG 289
 1446 TTTTCTGCTCTTTTATTTGCTGATCTGCTGTTCTTTGCGCGTTTCAGCTCATTTGTGTG- 1504
 290 TTTTCTGCTCTTTTACTTGTGTATAGTACTTTTCGGCCATTTCATGTTCTGTTGTGC 349
 1505 -CACCTCAGCTGAAAGTTGCTGCTACTTCTGTGGCTCTCGTGGCTGGCGGCGAGCTGCC 1563
 350 ACACATCATCTGAGAGCTCGTGTACCTCTGTAGCTCTCGTGGCTGGCGAGTGGAGGCA 409
 1564 TTT 1566
 410 TGT 412

RESULT 43
 BF442617
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Sus scrofa (pig)
 Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 460)
 Fahrenkrug S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R.,
 758 bp mRNA linear EST 20-JUN-2001
 602878836F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5010465 5',
 mRNA sequence.
 BI080925
 BI080925
 BI080925.1 GI:14499255
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 758)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

BF442617
 259515 MARC 2FIG Sus scrofa cDNA 5', mRNA sequence.
 ACCESSION
 BF442617
 VERSION
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Sus scrofa (pig)
 Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 460)
 Fahrenkrug S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R.,

RESULT 42
 BI080925
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 758)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

align44

Tue Sep 7 08:53:52 2004

Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
Location/Qualifiers
1..720
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

Query Match 4.6%; Score 110.4; DB 1; Length 720;
Best Local Similarity 82.9%; Pred. No. 0;
Matches 126; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 832 TCAGAGGAGAGAGAGCGCTTTACCAATTTCTGTTGTTGGTGGACCATGGCATG 891
DB 19 TTGTAGAGAGAGAACTCTTTGATCCCAATTTGCTGTTCTCTGTTGATCGGGCATG 78
QY 892 TCTGAACACAGGAAGTACGGGGCTCTCCACGAGGAGGTGAATACACCTCTGATTTA 951
DB 79 TCTGAACACTGGCTGATCGGGCTCTTCCATGAGGAGCTTACACCGCTGATCTTA 138
QY 952 ATCAGTTCTCGTTGTAAGAGAAACCGGTGA 983
DB 139 ATCAGTTCTGATTTGAAAGAAACCTGTGTA 170

RESULT 46
BE897861 934 bp mRNA linear EST 20-OCT-2000
LOCUS 601440532F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925494 5',
DEFINITION mRNA sequence.
ACCESSION BE897861
VERSION BE897861.1 GI:10363749
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 934)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC/DCTD/PTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: L1A9764 row: p column: 07
High quality sequence stop: 704.
Location/Qualifiers
1..934
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3925494"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_72"
/note="Organ: skin; Vector: pCMV-SPOrt6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

Query Match 4.5%; Score 108.4; DB 1; Length 934;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 120; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 832 TCAGAGGAGAGAGAGCGCTTTACCAATTTCTGTTGTTGGTGGACCATGGCATG 891
DB 19 TTGTAGAGAGAGAACTCTTTGATCCCAATTTGCTGTTCTCTGTTGATCGGGCATG 78
QY 892 TCTGAACACAGGAAGTACGGGGCTCTCCACGAGGAGGTGAATACACCTCTGATTTA 951
DB 79 TCTGAACACTGGCTGATCGGGCTCTTCCATGAGGAGCTTACACCGCTGATCTTA 138
QY 952 ATCAGTTCTCGTTGTAAGAGAAACCGGTGA 983
DB 139 ATCAGTTCTGATTTGAAAGAAACCTGTGTA 170

RESULT 47
BQ360060 122 bp mRNA linear EST 20-MAY-2002
LOCUS MR3-HN0166-310101-002-f02 HN0166 Homo sapiens cDNA, mRNA sequence.
DEFINITION BQ360060
ACCESSION BQ360060
VERSION BQ360060.1 GI:21028397
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 122)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202653
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&st2=MR3-HN0166-310101-002-f02&t3=2001-01-31&t4=1
Seq primer: puc 18 forward.
Location/Qualifiers
1..122
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HN0166"
/note="Organ: head normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Query Match 4.5%; Score 107.4; DB 1; Length 122;
Best Local Similarity 94.9%; Pred. No. 0;
Matches 111; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2271 CTGTGCCACGGTTGCACCTCGGGCCCATCTGGCTCATGCTCTCTCTCTGATTGAAT 2330
DB 5 CTCTGTGCAGCTTGCACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGATTGAAT 64

Best Local Similarity 53.9%; Pred. No. 0; Mismatches 187; Indels 0; Gaps 0; Matches 219; Conservative 0;

QY 403 GCAGAGCCACCTACAGTTACTATGCTCGATCAAGGCATTGATGAGCGGAGCTTCT 462
 Db 166 GCAGAGCCACCTACAGTTACTATGCTCGATCAAGGCATTGATGAGCGGAGCTTCT 225
 QY 463 GCTTTGTGAGCGTATCAGAACTCAATTTCTCTGCACTGCTGGAAGACAGTGTGATA 522
 Db 226 ACATTTGTAGATGTGGGTAGTAATTTGCCAGCTATGCCATCCCAAGAGGACATCTGATT 285
 QY 523 AGACAGCAAGAGAGCTGGAAGAAAGATAGTCTTTTATGAGATGAACCTGGGTAAA 582
 Db 286 CATCACTTTAGAGAACGGCAGAGAGTGGTCTTTATGAGCGATGACACTGGAGCGA 345
 QY 583 TTATTTCCAAAGCATTTTGTGGAATATGATGGAACAACTCTATTTTCTGCTGAGATAC 642
 Db 346 CTCCTTTCCAAAGAGTCTTCAAAATCTCTACTTTCTCCCTCTTAAATGTAAGGACCTT 405
 QY 643 ACAGAGGTGGATAAATAGTCAAGAGCATTTGGATAAAGTATTAAAGAGGAGATG 702
 Db 406 CACACTGTGGATAATGGGATCTACAGCACCTCTATCCCAAGGAGACAGTGGAGCTG 465
 QY 703 GACATATTATCTCCTACTACTGCGGCTGACACATGTCGCACATTTGAGGGCCCAAC 762
 Db 466 GATGTCATATTAGCCCACTCTCTGTTGTTGATGATCACTGTGGGCAAGAGCATGTCCCGAC 525
 QY 763 AGCCCCCTGATTGGGCAAGAGCTGAGCGAGATGACAGCGGTGCTGA 808
 Db 526 CACCCAGAGACTGCTAATAAATCGCACAGATGAACAGGTCTATCA 571

RESULT 50
 BM468049
 LOCUS
 DEFINITION AGENCOURT 6457533 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5577886
 5', mRNA sequence.
 ACCESSION BM468049
 VERSION
 KEYWORDS
 SOURCE EST. BM468049.1 GI:18517091
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 990)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: ATCC/DCDP/DRP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM12332 Row: a column: 23
 High quality sequence stop: 689.

FEATURES
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 1..990
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5577886"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC_72"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 2 kb. Library constructed by Life Technologies."

Query Match 4.3%; Score 103.1; DB 1; Length 990;
 Best Local Similarity 51.2%; Pred. No. 0; Mismatches 289; Conservative 0; Mismatches 249; Indels 21; Gaps 2;

QY 398 CTGAAGCAAGCCACCTACAGTTACTATGCTCGATCAAGGCATTGATGAGCGGAGCTTCT 457
 Db 36 CTAGGTTGACCTCTCTACACCATGCGAGGCTCAAGGCTCTACCACTGGCTCAC 95
 QY 458 TTCTGCTTTTGTGAGCGTATCAGAACTCAATTTCTCTGCACTGCTGGAAGACAGTGT 517
 Db 96 TGCTTACCTTTATGATGCTGGTAGTAATCTGCCAGCCAGCCATAGTGAAGACATC 155
 QY 518 TGATAGACAGCAAGCAAGCAGCTGGAAGAAAGATAGTCTTTTATGAGATGAACCTGGG 577
 Db 156 TCATTAGCAGCTACAGTGCAGGAGCGGTGATGTCATGAGGAGATGATACCTGGA 215
 QY 578 TTAATTTATCCAAAGCATTTTGTGGAATATGATGGAACAACTCTATTTTCTGCTGAG 637
 Db 216 AAGACCTTTTCCCTGGTCTTTCTCCAAAGCTTTCTTCTCCATCTTCAATGTGAG 275
 QY 638 ATTACACAGAGGTGGATAAATAGTCAAGGACATTTGGATAAAGTATTAAAGAGGAG 697
 Db 276 ACCTAGACAGTGGACATGCGATCTCTACCCACCATGGACAGTGGTG 335
 QY 698 ATTGGGACATATTATCTCTACTACCTGGGCTGGACACATTTGGCCACATTTGAGGG 757
 Db 336 AATGGGACGTGCTGATTGCTCTCTCTGGGTGTGGACCACTGTGGCCACCAAGCATGG 395
 QY 758 CCAACAGCCCCCTGATTGGGCAAGAGCTGAGCGAGATGACAGCGTGTGATGAGATCC 817
 Db 396 CTCACACCTCGAATGGCCAAAGAACTTAGCCAGATGAGCCAGGT-----GATCC 446
 QY 818 ACACCTACTGAGTGAAGGAGAGAGACGCCCTTTACCCAAATTTGCTGTTCTTTG 877
 Db 447 AGGACTTTGGAGCGCTCTGGAGAAATGACACAC-----TGCTGTAGTGGCTG 494
 QY 878 GTGACCATGCGCATGCTGAAACAGGAAAGTCAAGGGGCTCTCTCCACCGAGGAGTGAATA 937
 Db 495 GGGACCATGGATGACCAAAATGGAGACCATGGAGGGGACAGTGGAGGTCTCAT 554
 QY 938 CACTCTGATTTT 950
 Db 555 CTGCTCTCTTTCT 567

RESULT 51
 BM468049
 LOCUS
 DEFINITION BC036916 Homo sapiens, Similar to hypothetical protein MGC3079, clone IMAGE:5203414, mRNA.
 ACCESSION BC036916
 VERSION BC036916.1 GI:23331195
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2495)
 Strausberg, R.
 Direct Submission
 Submitted (23-AUG-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc.mcconhri.nih.gov
 Akhter N., Ayele K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghini, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Loric, P., Legaspi, R.,
 Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 78 Row: f Column: 8
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis

This clone has the following problem: frame shifted.

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FEATURES
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    1..2495
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      /db_xref="taxon:9606"
      /clone="IMAGE:5203414"
      /tissue_type="Lung, Spleen, fetal, pooled"
      /clone_lib="NIH MGC 122"
      /lab_host="DH10B"
      /note="Vector: pCMV-SPORT6"
  
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Query Match      4.3%; Score 103.1; DB 1; Length 2495;
Best Local Similarity 51.2%; Pred. No. 0;
Matches 283; Conservative 0; Mismatches 249; Indels 21; Gaps 2;

QY 398 CTGAAGCAAGACCACTACAGTTACTATGCTCGAATCAAGCATTGATGCGGGAGCC 457
Db 375 CTCAGGTTGACCTCTACACACCATGCGGCTCAAGCCCTCCACCTGCTCTAC 434
QY 458 TTCTGCTTTGTCGAGTCATCAGGAACCTCAATTTCTCTGACATGCTGGAAGACAGTG 517
Db 435 TGCTACTCTTTATGTGCTGGTAGTAATCTTCGCCAGCACGCCATAGTGGAGACAATC 494
QY 518 TGATAAGACAAAGCAAGCAGCTGGGAAAAGATAGTCTTTATGAGATGAACCTGGG 577
Db 495 TCATTAGCAGCTCACCAGTGCAGGAAGCGGTGTAGTCTTCATGGAGATGATACCTGGA 554
QY 578 TTAATTAATCCCAAGCATTGTGGAATATGATGGAACACCTCAATTTTCGTGTGAG 637
Db 555 AAGACCTTTTCCCTGGTGTCTTCCAAAGCTTTCTTCCCAAGCTTTCTTCCCAAGCTTTCAATGTCAGAG 614
QY 638 ATTACACAGAGGTGGAATAATATGTACAGGAGCATTTGGATAAAGTATTAAGAGAGGAG 697
Db 615 ACCTAGACAGTGGACATATGGCATCTCTGGAACACCTCTACCCACCATGGACAGTGTG 674
QY 698 ATTGGGACATTAATCTCCACTACTGGGCTGGACCAATGGCCACATTTTCAGGCG 757
Db 675 AATGGGACGTGCTGATGTCTACTTCTGGGTGGACCACTGTGGCCACAAGCATGGCC 734
QY 758 CCACAGCCCCCTGATTTGGGACAGAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCC 817
Db 735 CTCACCCCTGAAATGGCCAGAAATTTAGCCAGATGGACAGGT-----GATCC 785
QY 818 ACACCTCAGTCAGTCAAGAGAGAGAGCGCTTTTACCCATTTGCTGTGTTCTTTGTG 877
Db 786 AGGACCTTTGGAGCGTCTGAGAATGACACAC-----TGCTGGTAGTGGGTG 833
QY 878 GTGACCATGGCATGCTGAAACAGGAGTCAACGGGGCTCTCTCCACCGAGGAGGTGAATA 937
Db 834 GGGACCATGGGATGACCAACAAATGGAGACCATGAGGGGACAGTGAGCTGGAGTCTCAG 893
QY 938 CACTCTGATTTT 950
Db 894 CTGCTCTCTTTCT 906
  
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RESULT 52

AY408630

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

gene

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

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QY

Db

QY

Db

RESULT 56	AY408631	3270 bp	DNA	linear	GSS 12-DEC-2003
LOCUS	Pan troglodytes HCM3288 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
DEFINITION	AY408631				
ACCESSION	AY408631.1	GI:39764602			
VERSION	GSS.				
KEYWORDS	Pan troglodytes (chimpanzee)				
SOURCE	Pan troglodytes				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.				
REFERENCE	1. (bases 1 to 3270)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 3270)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	location/Qualifiers				
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	/organism="Pan troglodytes"				
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	/db_xref="taxon:9598"				
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	/locus_tag="HCM3288"				
gene					
Query Match					
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Matches 212; Conservative	0; Mismatches 197; Indels 0; Gaps 0;				
QY	398 CTGAAGCAAGCCACTACATGTTACTATGCTCGAATCAAGGCATTGATGACGGGAGCC	457			
Db	368 CTGAGTTGACCCCTCTTACCACCACTGAGCGCCTCAAGGCCCTCACCACCTGGCTCAC	427			
QY	458 TTCCTGGCTTTGTCGAGTCAATGAGCACTCAATTCCTCTGCTACTGCTGGAGACAGTGT	517			
Db	428 TGCCTACCTTTATTGATGCTGTGATGATTTGTCAGCCAGCCATAGTGAAGACAATC	487			
QY	518 TGATAGACAGCAAGACAGCTGGAAAAAGATAGTCTTTTATGGAGATGAACCTGGG	577			
Db	488 TCATTAAGCAGCTTACCAGTGCAGGAGGCGTGTAGTCTTCATGGGAGATGATACCTGGA	547			
QY	578 TTAATATTATCCCAAGCAATTTGTGGAATATGATGGAACAACCTCATTTTTCGTGTGAG	637			
Db	548 AAGACCTTTTCCCTGGTGTCTTCCAAAGCTTTCTTCTTCCCATCTTCAATGTGCAG	607			
QY	638 ATTACAGAGGTGGATAATATGTCAGGAGCATTTGGATAAGTATTAAAGAGGAG	697			
Db	608 ACCTAGACACAGTGGACAATGGCATCTGGACACCTTACCCCAACATGGACAGTGGTG	667			
QY	698 ATTGGACATATTATCTTCCACTCTGGGCTGGACCACATTTGGCCACATTTTCAGGCG	757			
Db	668 AATGGACGTGTGATTTGCTNANTTCTTGGTGTGGACCACTGTGGCCACAGCATGGCTG	727			
QY	758 CCAACAGCCCCCTGATTTGGGACAGAGCTCAGCAGATGACAGCGTGT	806			
Db	728 CTCACCACTGAAATGGCCAGAACNTNGCCAGATGACCAAGTGTAT	776			

align44

Tue Sep 7 08:53:52 2004

698 ATTGGGACATATTAACTCTCCACTACCTGGGCTGGACCAATTCGGCACATTTTCAGGCG 757
 309 CTGGGATGTCGTGATTCCTCACTTCCTGGGTGGATCAATTCGTGATTAAGCATGGCC 368
 758 CCAACAGCCCCCTGATTTGGGCGAGAGCTCAGCGAGATGACAGCGTGTCT 806
 369 CTCACCACTCTGAATGGCCAAAGAACTTAGCCAGATGACAGGATGAT 417

RESULT 58
 AY408632 3282 bp DNA linear GSS 12-DEC-2003
 LOCUS Mus musculus HCM3288 gene, VIRTUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY408632.1 GI:39764603
 VERSION AY408632.1
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 3282)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 3282)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
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 Best Local Similarity 51.3%; Pred. No. 0;
 Matches 210; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

398 CTGAAGCAAGCCACCTACAGTTACTGCTCGAATCAAGGCATTCATGACGGGAGCC 457
 368 CTCAGGTGGACCCCGCCAGCACCACCATGAGCGTCTAAGGCTCTCACCACCTGGCTGC 427
 458 TTCTGCTGCTTGTGCGAGTCTCATCAGAACCTCAATTCCTGCTGCTGGAAGACAGTG 517
 428 TGCCGACTTTCATTCATGCTGCGCAGTAACCTTTGCCAGCATGCTATAGTGAAGATATG 487
 518 TGATAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 577
 488 TCATCCACAGCTCAACAGCTGAGGAGGCGGTGAGTCTTCATGCGAGATGATACCTGGA 547
 578 TTAAATATTCCTCCAAAGCAATTTCTGGAATATGATGGAACAACCTCATTTTCGTGTGAG 637
 548 GAGACCTTTTCCCGGAGCTTTCTCAAGCTTTCTTCTCTCTCACTCTCAATGTCAGAG 607
 638 ATTACACAGAGTGGATTAATATGTCAGGAGCAATTTGGATAAGATTAATAAAGAGGAG 697
 608 ACCTGCACAGAGTGGATTAACCGCATCTTTGGAAACACCTCTATCTCTCCCTGGACGGGTT 667

AW862654 545 bp mRNA linear EST 19-MAY-2000
 RLF09 Rat Liver Subtracted cDNA Library Rattus norvegicus cDNA,
 mRNA sequence.
 AW862654
 AW862654.1 GI:7958365
 EST.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 545)
 Zhang, J., Underwood, L.E. and D'Ercole, A.J.
 Identification of fasting inducible genes from rat liver by
 suppression subtractive hybridization
 Unpublished (2000)
 Contact: Zhang Jihui
 Department of Pediatrics/Division of Endocrinology
 University of North Carolina Medical School
 509 Burnett-Womack Building, CB# 7220, Chapel Hill, NC 27599-7220,
 USA
 Tel: 919 966 4435
 Fax: 919 966 2423
 Email: jihui.zhang@med.unc.edu.
 Location/Qualifiers
 1..545
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /sex="male"
 /dev_stage="five-week-old postnatal, fasting for 48 hours"
 /clone_lib="Rat Liver Subtracted cDNA Library"
 /note="Organ: liver; Vector: pGEM-T; This subtracted cDNA
 library was constructed by inserting desired
 differentially expressed sequences into a plasmid pGEM-T,
 followed by transforming E. coli strain JM109.
 Differentially expressed sequences from fasted rat liver
 were generated by suppression subtractive hybridization,
 in which mRNA from fasted rats was used as a test and
 mRNA from control fed rats as a reference. A standard
 tailing procedure with Taq DNA polymerase was employed to
 introduce 3'-A overhang to the desired cDNAs before
 cloning into pGEM-T. Subtraction efficiency of this
 library was shown to be >60%. The average insert size of
 clones in this library is 369 bp (20 bp)."

Query Match 3.9%; Score 93.8002; DB 1; Length 545;
 Best Local Similarity 51.8%; Pred. No. 0;
 Matches 212; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

398 CTGAAGCAAGCCACCTACAGTTACTGCTCGAATCAAGGCATTCATGACGGGAGCC 457
 9 CTCAGGTGGATCCCGCCAGCACCACCATGAGCGTCTGAGGCTCTCACCCTGGCTGC 68
 458 TTCTGCTGCTTGTGCGAGTCTCATCAGAACCTCAATTCCTGCTGCTGGAAGACAGTG 517
 69 TGCCGACTTTCATTCATGCTGCGCAGTAACCTTCGCCAGCATGCTATTCGTGAAGATATC 128
 518 TGATAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 577
 129 TCATCAAGCAGCTCACCAGTGCAGGAACCGGTGATCTTCATGCGAGATGATACCTGGA 188
 578 TTAAATATTCCTCCAAAGCAATTTCTGGAATATGATGGAACAACCTCATTTTCGTGTGAG 637
 189 GAGACCTTTTCCCTGGAGCATTTTCCCAAGCTTTCTTCTCTCTCACTCTCAATGTCAGAG 248
 638 ATTACACAGAGTGGATTAATATGTCAGGAGCAATTTGGATAAGATTAATAAAGAGGAG 697
 249 ACCTGCACAGAGTGGATTAACCGCATCTTTGGAAACACCTCTATCTCTCCCTGGACGGG 308

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QY 598 ATTGGGACATATTAACTCTCCACTACTGCGGTGGACCACTTGGCCACATTTCAGGGC 757
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668 CGTGGGATGTGCTGATCGCTCACTTCTCTGCTGGATCACTGTGGTCAACACAGCGCC 727
QY 758 CCAACAGCCCCCTGATTGGCAGAGCTGAGCGAGATGGACACGCTGCT 806
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
728 CTCACACCTGAAATGGCCAGAGAACTTAGCCAGATGGACCAAGTGTAT 776

RESULT 59
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DEFINITION 187887 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE685541
VERSION BE685541.1 GI:10073165
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 124)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A.,
Chitko-McKown, C.G., Pettea, G., Holt, I., Karameycheva, S., Liang, F.,
Quackenbush, J., and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 628-630 (2001)
21180013
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCCGATCAGCAGC
Plate: 100 row: 0 column: 19
Seq primer: ATTAGGTGACACTATAG.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4BOV"
/notes="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 20 and day 40
embryos."
Query Match 3.7%; Score 89; DB 1; Length 124;
Best Local Similarity 83.5%; Pred. No. 0;
Matches 101; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1172 ATGTGCGGTCATATGAAAGATCTCTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGC 1231
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 ATGTTCCATCATACAACAAGAGCCTGGATTGGACGAGTTTAAAGTGTGCGAAAGATCGC 60
QY 1232 ATGGGAACTGGATCAGATCTGTACTGGAGGAAAGCAATTCAGAGTCCTATTCAACCTGG 1291
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 ACAGAAACTGGATCAGATCTGTACTGGAGGAAAGCAATTCAGAGTCCTATTCAACCTGG 1291
QY 1292 G 1292
Db 121 G 121

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RESULT 60

CD733602

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..140

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="white leghorn SC"

/db_xref="taxon:9031"

/clone_lib="IGAL_50C03"

/sex="mixed"

/tissue_type="Gut"

/cell_type="Lymphocyte"

/dev_stage="Adult"

/lab_host="EMDH10B"

/clone_lib="IGAL - Chicken Intestinal Lymphocyte"

/notes="Organ: Intestine; Vector: pCMV-SPORT6; Site 1:

SalI; Site 2: NotI; Normalized library from chicken gut

infected with coccidia duodenum and middle gut."

Query Match 3.7%; Score 87.8; DB 1; Length 140;

Best Local Similarity 77.0%; Pred. No. 0;

Matches 107; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1148 AGCTTAGTAACTGTGTCAGAGAAATGTCCTCATATCAAAAAGATCTGGTTTGAGC 1207

Db 1 AACTTAGCACACTGTGTGCAAGAGATACACCCGCTATGAAAAGATCTTTGATTGAGC 60

QY 1208 AGTTTAAATGTCAAGAAAGATTGCATGGGAATTCAGATCGATCTTGGAGGAAAGC 1267

Db 61 AGTTTAAAGATAGACAGAAAGTCCCATGGCACTGGATCAACTGATCTGCTGGAGGGAATA 120

QY 1268 ATTCAAGAGTCTTATTCAA 1286

Db 121 ATTCAAGATACTCTTAAA 139

Search completed: September 7, 2004, 08:52:24

Job time : 63 secs

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